SEQ SEARCH SUMMARY

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 35.988 Seconds
                                              (without alignments)
                                              1975.923 Million cell updates/sec

Title: US-09-674-330A-3
Perfect score: 2536
Sequence: 1 MPGLKRILTVTILALWLPHP..........INFRGSSVIRLRIYVSQYPF 448

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_19Jun03:*
                 1:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
                 2:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
                 3:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
                 4:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
                 5:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
                 6:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
                 7:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
                 8:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
                 9:   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
                 10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
                 11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
                 12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
                 13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
                 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
                 15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
                 16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
                 17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
                 18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
                 19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
                 20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
                 21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
                 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
                 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
                 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID		Description
1	2536	100.0	448	21	AAY56750	*Appl.* ωo	Smooth muscle prol
2	2536	100.0	448	21	AAY54990	"	Full length mouse
3	2505	98.8	461	21	AAY56752	"	Smooth muscle prol
4	2505	98.8	461	21	AAY54991	"	Full length mouse
5	2405	94.8	448	19	AAW79739		(Human) EEGF protein
6	2405	94.8	448	20	AAW95709		Homo sapiens fetal
7	2405	94.8	448	20	AAW94281		Human extracellula
8	2405	94.8	448	21	AAY57058		Amino acid sequenc
9	2405	94.8	448	21	AAY54989		Full length human
10	2405	94.8	448	22	AAM93573		Human polypeptide,
11	2405	94.8	448	23	AAU75494		Human extracellula
12	2403	94.8	423	21	AAY56751		Smooth muscle prol
13	2403	94.8	423	21	AAY56753		Smooth muscle prol
14	2399	94.6	448	20	AAY08063		Human EGF-like hom
15	2399	94.6	448	22	AAU29227		Human PRO polypept
16	2399	94.6	448	22	AAB31183		Amino acid sequenc
17	2399	94.6	448	24	ABU71315		Human PRO210 prote
18	2399	94.6	448	24	ABU72040		Novel human secret
19	2399	94.6	448	24	ABU65772		Human secreted/tra
20	2399	94.6	448	24	ABU66105		Novel human secret
21	2399	94.6	448	24	ABU67141		Novel human secret
22	2399	94.6	448	24	ABU67272		Novel human secret
23	2399	94.6	448	24	ABU67609		Human secreted/tra
24	2399	94.6	448	24	ABU65467		Human PRO polypept
25	2399	94.6	448	24	ABU58603		Human PRO polypept
26	2399	94.6	448	24	ABU56139		Human secreted/tra
27	2399	94.6	448	24	ABU57134		Human PRO polypept
28	2399	94.6	448	24	ABU10713		Human secreted/tra
29	2125	83.8	392	18	AAW31705		Human extracellula
30	1869	73.7	335	21	AAY76008		Rat EGF extracellu
31	1869	73.7	335	22	AAB55947		Skin cell protein,
32	1869	73.7	335	23	ABB72147		Rat protein isolat
33	1275	50.3	443	18	AAW32110		Human extracellula
34	1275	50.3	443	20	AAY16587		Extracellular prot
35	1275	50.3	443	21	AAB33418		Human PRO226 prote
36	1275	50.3	443	21	AAY84707		A human p53 mutant
37	1275	50.3	443	21	AAY55850		Human S1-5 ECMP-li
38	1275	50.3	443	22	AAU12330		Human PRO226 polyp
39	1275	50.3	443	23	AAU86130		Human PRO226 polyp
40	1275	50.3	443	24	ABU66728		Human PRO polypept
41	1275	50.3	443	24	ABU67004		Human secreted/tra
42	1275	50.3	443	24	ABU59809		Novel secreted and
43	1271	50.1	443	22	AAB92533		Human protein sequ
44	1260	49.7	443	21	AAY84706		Amino acid sequenc
45	1225.5	48.3	433	21	AAB58353		Lung cancer associ

ALIGNMENTS

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:01:28 ; Search time 15.1351 Seconds
                                              (without alignments)
                                              1252.401 Million cell updates/sec

Title: US-09-674-330A-3
Perfect score: 2536
Sequence: 1 MPGLKRILTVTILALWLPHP..........INFRGSSVIRLRIYVSQYPF 448

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
                  1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                  2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                  3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                  4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                  5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                  6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
  No.   Score   Match Length DB   ID   Description
----
     1   2405   94.8   448   2   US-08-884-072-1   Sequence 1, Appli
     2   2405   94.8   448   4   US-09-212-168-1   Sequence 1, Appli
     3   1869   73.7   335   4   US-09-312-283C-186   Sequence 186, App
     4   1832   72.2   337   3   US-09-188-930-186   Sequence 186, App
     5   1275   50.3   443   2   US-08-833-963C-2   Sequence 2, Appli
     6   1275   50.3   443   3   US-08-980-514-1   Sequence 1, Appli
     7   966.5   38.1   387   2   US-08-884-072-5   Sequence 5, Appli
     8   966.5   38.1   387   2   US-08-833-963C-9   Sequence 9, Appli
     9   966.5   38.1   387   3   US-08-980-514-3   Sequence 3, Appli
    10   966.5   38.1   387   4   US-09-212-168-5   Sequence 5, Appli
    11   897.5   35.4   274   3   US-09-188-930-336   Sequence 336, App

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OM protein - protein search, using sw model

Run on:          December 12, 2003, 10:05:03 ; Search time 26.2342 Seconds
                                            (without alignments)
                                            3176.029 Million cell updates/sec

Title:           US-09-674-330A-3
Perfect score:   2536
Sequence:        1 MPGLKRILTVTILALWLPHP..........INFRGSSVIRLRIYVSQYPF 448

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters:      684280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_AA:*
                 1:  /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                 2:  /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                 3:  /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                 4:  /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
                 5:  /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                 6:  /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
                 7:  /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                 8:  /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                 9:  /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
                 10:  /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
                 11:  /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
                 12:  /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                 13:  /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                 14:  /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                 15:  /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
                 16:  /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                 17:  /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
                 18:  /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
```

```
                                SUMMARIES
                        %
Result              Query
   No.    Score   Match  Length  DB   ID                        Description
        -------------------------------------------------------------------------
      1    2405    94.8    448    9   US-09-083-002-2           Sequence 2, Appli
      2    2405    94.8    448    9   US-09-275-805-2           Sequence 2, Appli
      3    2405    94.8    448    9   US-09-836-561-1           Sequence 1, Appli
      4    2405    94.8    448   14   US-10-041-016-2           Sequence 2, Appli
      5    2399    94.6    448   12   US-10-199-672-408         Sequence 408, App
      6    2399    94.6    448   12   US-10-187-749-408         Sequence 408, App
      7    2399    94.6    448   12   US-10-194-457-408         Sequence 408, App
      8    2399    94.6    448   12   US-10-184-642-408         Sequence 408, App
      9    2399    94.6    448   12   US-10-196-747-408         Sequence 408, App
     10    2399    94.6    448   12   US-10-173-689-408         Sequence 408, App
     11    2399    94.6    448   12   US-10-173-690-408         Sequence 408, App
     12    2399    94.6    448   12   US-10-173-691-408         Sequence 408, App
     13    2399    94.6    448   12   US-10-173-692-408         Sequence 408, App
     14    2399    94.6    448   12   US-10-173-694-408         Sequence 408, App
     15    2399    94.6    448   12   US-10-173-698-408         Sequence 408, App
     16    2399    94.6    448   12   US-10-173-699-408         Sequence 408, App
     17    2399    94.6    448   12   US-10-173-707-408         Sequence 408, App
     18    2399    94.6    448   12   US-10-174-569-408         Sequence 408, App
     19    2399    94.6    448   12   US-10-174-583-408         Sequence 408, App
     20    2399    94.6    448   12   US-10-174-587-408         Sequence 408, App
     21    2399    94.6    448   12   US-10-174-589-408         Sequence 408, App
     22    2399    94.6    448   12   US-10-174-591-408         Sequence 408, App
     23    2399    94.6    448   12   US-10-175-736-408         Sequence 408, App
     24    2399    94.6    448   12   US-10-175-742-408         Sequence 408, App
     25    2399    94.6    448   12   US-10-175-744-408         Sequence 408, App
     26    2399    94.6    448   12   US-10-175-745-408         Sequence 408, App
     27    2399    94.6    448   12   US-10-175-748-408         Sequence 408, App
     28    2399    94.6    448   12   US-10-175-751-408         Sequence 408, App
     29    2399    94.6    448   12   US-10-175-754-408         Sequence 408, App
     30    2399    94.6    448   12   US-10-176-480-408         Sequence 408, App
     31    2399    94.6    448   12   US-10-176-489-408         Sequence 408, App
     32    2399    94.6    448   12   US-10-176-754-408         Sequence 408, App
     33    2399    94.6    448   12   US-10-176-755-408         Sequence 408, App
     34    2399    94.6    448   12   US-10-176-759-408         Sequence 408, App
     35    2399    94.6    448   12   US-10-176-920-408         Sequence 408, App
     36    2399    94.6    448   12   US-10-176-922-408         Sequence 408, App
     37    2399    94.6    448   12   US-10-176-924-408         Sequence 408, App
     38    2399    94.6    448   12   US-10-176-984-408         Sequence 408, App
     39    2399    94.6    448   12   US-10-179-508-408         Sequence 408, App
     40    2399    94.6    448   12   US-10-179-512-408         Sequence 408, App
     41    2399    94.6    448   12   US-10-179-515-408         Sequence 408, App
     42    2399    94.6    448   12   US-10-066-198-15          Sequence 15, Appl
     43    2399    94.6    448   12   US-10-173-702-408         Sequence 408, App
     44    2399    94.6    448   12   US-10-173-703-408         Sequence 408, App
     45    2399    94.6    448   12   US-10-173-704-408         Sequence 408, App


                                ALIGNMENTS


RESULT 1
US-09-083-002-2
```

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 14.1261 Seconds
                                              (without alignments)
                                              3049.921 Million cell updates/sec

Title: US-09-674-330A-3
Perfect score: 2536
Sequence: 1 MPGLKRILTVTILALWLPHP..........INFRGSSVIRLRIYVSQYPF 448

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_76:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1119.5	44.1	493	2	JC5621	epidermal growth f
2	966.5	38.1	387	2	I38449	extracellular prot
3	764.5	30.1	1221	2	A49457	fibulin-2 precurso
4	736.5	29.0	1184	2	A55184	fibulin-2 precurso
5	733.5	28.9	685	2	S78040	fibulin, splice fo
6	729.5	28.8	683	2	C36346	fibulin 1 precurso
7	688	27.1	705	2	S34968	fibulin, splice fo
8	613.5	24.2	601	2	B36346	fibulin 1 precurso
9	608	24.0	689	2	T42760	fibulin, splice fo
10	600	23.7	712	2	T42990	fibulin 1, splice
11	597.5	23.6	589	2	T43210	fibulin-1D precurs
12	573	22.6	798	2	T22793	hypothetical prote
13	537	21.2	1394	2	A35626	transforming growt

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 9.08108 Seconds
                                            (without alignments)
                                            2319.984 Million cell updates/sec

Title: US-09-674-330A-3
Perfect score: 2536
Sequence: 1 MPGLKRILTVTILALWLPHP..........INFRGSSVIRLRIYVSQYPF 448

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SwissProt_41:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
  No.   Score Match Length DB   ID   Description
----
     1   2536 100.0   448   1   FBL5_MOUSE   *lata*   Q9wvh9 mus musculu
     2   2500   98.6   448   1   FBL5_RAT   *late*   Q9wvh8 rattus norv
     3   2405   94.8   448   1   FBL5_HUMAN   Q9ubx5 homo sapien
     4   1275   50.3   443   1   FBL4_HUMAN   O95967 homo sapien
     5   1269   50.0   443   1   FBL4_CRIGR   O55058 cricetulus
     6   1260   49.7   443   1   FBL4_MOUSE   Q9wvj9 mus musculu
     7   1119.5   44.1   493   1   FBL3_RAT   O35568 rattus norv
     8   1104   43.5   493   1   FBL3_HUMAN   Q12805 homo sapien
     9   764.5   30.1   1221   1   FBL2_MOUSE   P37889 mus musculu
    10   736.5   29.0   1184   1   FBL2_HUMAN   P98095 homo sapien
    11   722   28.5   704   1   FBL1_CHICK   O73775 gallus gall
    12   711   28.0   598   1   FBL1_CERAE   Q8mjj9 cercopithec
    13   695   27.4   703   1   FBL1_HUMAN   P23142 homo sapien
    14   685   27.0   705   1   FBL1_MOUSE   Q08879 mus musculu
    15   654.5   25.8   681   1   FBL1_BRARE   O42182 brachydanio
    16   573   22.6   798   1   FBL1_CAEEL   O77469 caenorhabdi
    17   537   21.2   1394   1   LTBS_HUMAN   P22064 homo sapien

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 30.6066 Seconds
                                              (without alignments)
                                              3777.210 Million cell updates/sec

Title: US-09-674-330A-3
Perfect score: 2536
Sequence: 1 MPGLKRILTVTILALWLPHP..........INFRGSSVIRLRIYVSQYPF 448

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SPTREMBL_23:*
                1: sp_archea:*
                2: sp_bacteria:*
                3: sp_fungi:*
                4: sp_human:*
                5: sp_invertebrate:*
                6: sp_mammal:*
                7: sp_mhc:*
                8: sp_organelle:*
                9: sp_phage:*
               10: sp_plant:*
               11: sp_rodent:*
               12: sp_virus:*
               13: sp_vertebrate:*
               14: sp_unclassified:*
               15: sp_rvirus:*
               16: sp_bacteriap:*
               17: sp_archeap:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1275	50.3	443	4	Q96TF5	Q96tf5 homo sapien
2	1261	49.7	443	11	Q9JM06	Q9jm06 mus musculu
3	1252	49.4	443	4	Q9H3D5	Q9h3d5 homo sapien
4	1109	43.7	493	11	Q8BPB5	Q8bpb5 mus musculu
5	967	38.1	387	11	Q8K0J4	Q8k0j4 mus musculu
6	767.5	30.3	1174	11	Q99K58	Q99k58 mus musculu
7	738.5	29.1	576	4	Q9Y3V7	Q9y3v7 homo sapien
8	737.5	29.1	1231	4	Q8IUI1	Q8iui1 homo sapien
9	736.5	29.0	1231	4	Q8IUI0	Q8iui0 homo sapien
10	730.5	28.8	685	11	Q922K8	Q922k8 mus musculu
11	730.5	28.8	685	11	Q8C3B1	Q8c3b1 mus musculu
12	729.5	28.8	683	4	Q8TBH8	Q8tbh8 homo sapien
13	722	28.5	704	13	O73774	O73774 gallus gall
14	711	28.0	598	6	Q8MJJ9	Q8mjj9 cercopithec
15	690	27.2	638	4	Q8NBH6	Q8nbh6 homo sapien
16	664.5	26.2	495	4	Q9HBQ5	Q9hbq5 homo sapien
17	654.5	25.8	681	13	O42182	O42182 brachydanio
18	620	24.4	698	5	Q9V4B8	Q9v4b8 drosophila
19	577.5	22.8	554	4	Q9UH16	Q9uh16 homo sapien
20	561	22.1	1409	5	Q9VS89	Q9vs89 drosophila
21	557	22.0	2673	4	Q96SC3	Q96sc3 homo sapien
22	546	21.5	5636	4	Q96RW7	Q96rw7 homo sapien
23	527.5	20.8	2872	11	Q9WUH8	Q9wuh8 rattus norv
24	527	20.8	3857	11	O88840	O88840 mus musculu
25	524.5	20.7	1398	13	Q8AXM6	Q8axm6 xenopus lae
26	524.5	20.7	1399	13	Q8JFZ4	Q8jfz4 xenopus lae
27	524.5	20.7	2809	4	Q96JP8	Q96jp8 homo sapien
28	520.5	20.5	741	4	Q96K89	Q96k89 homo sapien
29	515	20.3	1389	11	Q8CG18	Q8cg18 mus musculu
30	515	20.3	1713	11	Q8CG19	Q8cg19 mus musculu
31	514	20.3	188	11	Q8R1U8	Q8r1u8 mus musculu
32	513.5	20.2	2906	11	Q9WUH9	Q9wuh9 rattus norv
33	512.5	20.2	787	11	Q8K061	Q8k061 mus musculu
34	511	20.1	1713	11	O88349	O88349 mus musculu
35	509.5	20.1	708	13	P87363	P87363 gallus gall
36	503.5	19.9	937	5	Q9BLJ1	Q9blj1 ciona intes
37	495.5	19.5	729	11	Q8BNH3	Q8bnh3 mus musculu
38	492.5	19.4	746	4	Q96HB9	Q96hb9 homo sapien
39	492.5	19.4	893	6	Q8MJK0	Q8mjk0 cercopithec
40	492.5	19.4	1256	4	Q9NS15	Q9ns15 homo sapien
41	492.5	19.4	1382	4	Q9H7K2	Q9h7k2 homo sapien
42	492	19.4	1289	5	Q8SSS3	Q8sss3 dictyosteli
43	492	19.4	1963	6	Q28019	Q28019 bos taurus
44	489.5	19.3	1062	11	Q60789	Q60789 mus musculu
45	485.5	19.1	1764	11	O35806	O35806 rattus norv

ALIGNMENTS

RESULT 1
Q96TF5

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 37.0323 Seconds
                                              (without alignments)
                                              1975.923 Million cell updates/sec

Title: US-09-674-330A-8
Perfect score: 2610
Sequence: 1 MGPRSFEPMHSGLCRQRRMI..........INFRGSSVIRLRIYVSQYPF 461

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_19Jun03:*
                 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
                 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
                 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
                 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
                 5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
                 6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
                 7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
                 8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
                 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
                 10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
                 11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
                 12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
                 13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
                 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
                 15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
                 16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
                 17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
                 18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
                 19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
                 20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
                 21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
                 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
                 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
                 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2610	100.0	461	21	AAY56752	Smooth muscle prol
2	2610	100.0	461	21	AAY54991	Full length mouse
3	2505	96.0	448	21	AAY56750	Smooth muscle prol
4	2505	96.0	448	21	AAY54990	Full length mouse
5	2403	92.1	423	21	AAY56751	Smooth muscle prol
6	2403	92.1	423	21	AAY56753	Smooth muscle prol
7	2376	91.0	448	19	AAW79739	Human EEGF protein
8	2376	91.0	448	20	AAW95709	Homo sapiens fetal
9	2376	91.0	448	20	AAW94281	Human extracellula
10	2376	91.0	448	21	AAY57058	Amino acid sequenc
11	2376	91.0	448	21	AAY54989	Full length human
12	2376	91.0	448	22	AAM93573	Human polypeptide,
13	2376	91.0	448	23	AAU75494	Human extracellula
14	2370	90.8	448	20	AAY08063	Human EGF-like hom
15	2370	90.8	448	22	AAU29227	Human PRO polypept
16	2370	90.8	448	22	AAB31183	Amino acid sequenc
17	2370	90.8	448	24	ABU71315	Human PRO210 prote
18	2370	90.8	448	24	ABU72040	Novel human secret
19	2370	90.8	448	24	ABU65772	Human secreted/tra
20	2370	90.8	448	24	ABU66105	Novel human secret
21	2370	90.8	448	24	ABU67141	Novel human secret
22	2370	90.8	448	24	ABU67272	Novel human secret
23	2370	90.8	448	24	ABU67609	Human secreted/tra
24	2370	90.8	448	24	ABU65467	Human PRO polypept
25	2370	90.8	448	24	ABU58603	Human PRO polypept
26	2370	90.8	448	24	ABU56139	Human secreted/tra
27	2370	90.8	448	24	ABU57134	Human PRO polypept
28	2370	90.8	448	24	ABU10713	Human secreted/tra
29	2125	81.4	392	18	AAW31705	Human extracellula
30	1869	71.6	335	21	AAY76008	Rat EGF extracellu
31	1869	71.6	335	22	AAB55947	Skin cell protein,
32	1869	71.6	335	23	ABB72147	Rat protein isolat
33	1268	48.6	443	18	AAW32110	Human extracellula
34	1268	48.6	443	20	AAY16587	Extracellular prot
35	1268	48.6	443	21	AAB33418	Human PRO226 prote
36	1268	48.6	443	21	AAY84707	A human p53 mutant
37	1268	48.6	443	21	AAY55850	Human S1-5 ECMP-li
38	1268	48.6	443	22	AAU12330	Human PRO226 polyp
39	1268	48.6	443	23	AAU86130	Human PRO226 polyp
40	1268	48.6	443	24	ABU66728	Human PRO polypept
41	1268	48.6	443	24	ABU67004	Human secreted/tra
42	1268	48.6	443	24	ABU59809	Novel secreted and
43	1264	48.4	443	22	AAB92533	Human protein sequ
44	1257	48.2	443	21	AAY84706	Amino acid sequenc
45	1225.5	47.0	433	21	AAB58353	Lung cancer associ

Appl. _wo_

ALIGNMENTS

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:01:28 ; Search time 15.5743 Seconds
                                        (without alignments)
                                        1252.401 Million cell updates/sec

Title: US-09-674-330A-8
Perfect score: 2610
Sequence: 1 MGPRSFEPMHSGLCRQRRMI..........INFRGSSVIRLRIYVSQYPF 461

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
                1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

| | | % | | | | |
Result No.	Score	Query Match	Length	DB	ID	Description
1	2376	91.0	448	2	US-08-884-072-1	Sequence 1, Appli
2	2376	91.0	448	4	US-09-212-168-1	Sequence 1, Appli
3	1869	71.6	335	4	US-09-312-283C-186	Sequence 186, App
4	1832	70.2	337	3	US-09-188-930-186	Sequence 186, App
5	1268	48.6	443	2	US-08-833-963C-2	Sequence 2, Appli
6	1268	48.6	443	3	US-08-980-514-1	Sequence 1, Appli
7	966.5	37.0	387	2	US-08-884-072-5	Sequence 5, Appli
8	966.5	37.0	387	2	US-08-833-963C-9	Sequence 9, Appli
9	966.5	37.0	387	3	US-08-980-514-3	Sequence 3, Appli
10	966.5	37.0	387	4	US-09-212-168-5	Sequence 5, Appli
11	897.5	34.4	274	3	US-09-188-930-336	Sequence 336, App

OM protein - protein search, using sw model

Run on: December 12, 2003, 10:05:03 ; Search time 26.9955 Seconds
                                          (without alignments)
                                          3176.029 Million cell updates/sec

Title: US-09-674-330A-8
Perfect score: 2610
Sequence: 1 MGPRSFEPMHSGLCRQRRMI..........INFRGSSVIRLRIYVSQYPF 461

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA:*
         1:   /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
         2:   /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
         3:   /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
         4:   /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
         5:   /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
         6:   /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
         7:   /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
         8:   /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
         9:   /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
        10:   /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
        11:   /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
        12:   /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
        13:   /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
        14:   /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
        15:   /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
        16:   /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
        17:   /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
        18:   /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

```
                              SUMMARIES
                        %
Result              Query
   No.    Score    Match  Length  DB   ID                      Description
      --------------------------------------------------------------------------
         1    2376    91.0     448    9   US-09-083-002-2         Sequence 2, Appli
         2    2376    91.0     448    9   US-09-275-805-2         Sequence 2, Appli
         3    2376    91.0     448    9   US-09-836-561-1         Sequence 1, Appli
         4    2376    91.0     448   14   US-10-041-016-2         Sequence 2, Appli
         5    2370    90.8     448   12   US-10-199-672-408       Sequence 408, App
         6    2370    90.8     448   12   US-10-187-749-408       Sequence 408, App
         7    2370    90.8     448   12   US-10-194-457-408       Sequence 408, App
         8    2370    90.8     448   12   US-10-184-642-408       Sequence 408, App
         9    2370    90.8     448   12   US-10-196-747-408       Sequence 408, App
        10    2370    90.8     448   12   US-10-173-689-408       Sequence 408, App
        11    2370    90.8     448   12   US-10-173-690-408       Sequence 408, App
        12    2370    90.8     448   12   US-10-173-691-408       Sequence 408, App
        13    2370    90.8     448   12   US-10-173-692-408       Sequence 408, App
        14    2370    90.8     448   12   US-10-173-694-408       Sequence 408, App
        15    2370    90.8     448   12   US-10-173-698-408       Sequence 408, App
        16    2370    90.8     448   12   US-10-173-699-408       Sequence 408, App
        17    2370    90.8     448   12   US-10-173-707-408       Sequence 408, App
        18    2370    90.8     448   12   US-10-174-569-408       Sequence 408, App
        19    2370    90.8     448   12   US-10-174-583-408       Sequence 408, App
        20    2370    90.8     448   12   US-10-174-587-408       Sequence 408, App
        21    2370    90.8     448   12   US-10-174-589-408       Sequence 408, App
        22    2370    90.8     448   12   US-10-174-591-408       Sequence 408, App
        23    2370    90.8     448   12   US-10-175-736-408       Sequence 408, App
        24    2370    90.8     448   12   US-10-175-742-408       Sequence 408, App
        25    2370    90.8     448   12   US-10-175-744-408       Sequence 408, App
        26    2370    90.8     448   12   US-10-175-745-408       Sequence 408, App
        27    2370    90.8     448   12   US-10-175-748-408       Sequence 408, App
        28    2370    90.8     448   12   US-10-175-751-408       Sequence 408, App
        29    2370    90.8     448   12   US-10-175-754-408       Sequence 408, App
        30    2370    90.8     448   12   US-10-176-480-408       Sequence 408, App
        31    2370    90.8     448   12   US-10-176-489-408       Sequence 408, App
        32    2370    90.8     448   12   US-10-176-754-408       Sequence 408, App
        33    2370    90.8     448   12   US-10-176-755-408       Sequence 408, App
        34    2370    90.8     448   12   US-10-176-759-408       Sequence 408, App
        35    2370    90.8     448   12   US-10-176-920-408       Sequence 408, App
        36    2370    90.8     448   12   US-10-176-922-408       Sequence 408, App
        37    2370    90.8     448   12   US-10-176-924-408       Sequence 408, App
        38    2370    90.8     448   12   US-10-176-984-408       Sequence 408, App
        39    2370    90.8     448   12   US-10-179-508-408       Sequence 408, App
        40    2370    90.8     448   12   US-10-179-512-408       Sequence 408, App
        41    2370    90.8     448   12   US-10-179-515-408       Sequence 408, App
        42    2370    90.8     448   12   US-10-066-198-15        Sequence 15, Appl
        43    2370    90.8     448   12   US-10-173-702-408       Sequence 408, App
        44    2370    90.8     448   12   US-10-173-703-408       Sequence 408, App
        45    2370    90.8     448   12   US-10-173-704-408       Sequence 408, App


                              ALIGNMENTS



RESULT 1
US-09-083-002-2
```

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 14.536 Seconds
                                          (without alignments)
                                          3049.921 Million cell updates/sec

Title: US-09-674-330A-8
Perfect score: 2610
Sequence: 1 MGPRSFEPMHSGLCRQRRMI..........INFRGSSVIRLRIYVSQYPF 461

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_76:*
                1: pir1:*
                2: pir2:*
                3: pir3:*
                4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score Match Length DB ID   Description
----
     1 1119.5   42.9   493 2   JC5621   epidermal growth f
     2   966.5   37.0   387 2   I38449   extracellular prot
     3   764.5   29.3   1221 2   A49457   fibulin-2 precurso
     4   736.5   28.2   1184 2   A55184   fibulin-2 precurso
     5   733.5   28.1   685 2   S78040   fibulin, splice fo
     6   729.5   28.0   683 2   C36346   fibulin 1 precurso
     7   688   26.4   705 2   S34968   fibulin, splice fo
     8   613.5   23.5   601 2   B36346   fibulin 1 precurso
     9   608   23.3   689 2   T42760   fibulin, splice fo
    10   600   23.0   712 2   T42990   fibulin 1, splice
    11   597.5   22.9   589 2   T43210   fibulin-1D precurs
    12   573   22.0   798 2   T22793   hypothetical prote
    13   537   20.6   1394 2   A35626   transforming growt

```
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OM protein - protein search, using sw model

Run on:         December 12, 2003, 10:00:22 ; Search time 9.34459 Seconds
                                            (without alignments)
                                            2319.984 Million cell updates/sec


Title:          US-09-674-330A-8
Perfect score:  2610
Sequence:       1 MGPRSFEPMHSGLCRQRRMI.........INFRGSSVIRLRIYVSQYPF 461


Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5


Searched:       127863 seqs, 47026705 residues


Total number of hits satisfying chosen parameters:      127863


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :      SwissProt_41:*


       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.


                              SUMMARIES
                       %
Result              Query
   No.    Score   Match Length DB   ID                      Description
------------------------------------------------------------------------------
     1     2505   96.0     448  1   FBL5_MOUSE    LATE    (Q9wvh9)mus musculu 1999 ART
     2     2469   94.6     448  1   FBL5_RAT              Q9wvh8 rattus norv
     3     2376   91.0     448  1   FBL5_HUMAN            Q9ubx5 homo sapien
     4     1268   48.6     443  1   FBL4_HUMAN            O95967 homo sapien
     5     1262   48.4     443  1   FBL4_CRIGR            O55058 cricetulus
     6     1257   48.2     443  1   FBL4_MOUSE            Q9wvj9 mus musculu
     7   1119.5   42.9     493  1   FBL3_RAT              O35568 rattus norv
     8     1103   42.3     493  1   FBL3_HUMAN            Q12805 homo sapien
     9    764.5   29.3    1221  1   FBL2_MOUSE            P37889 mus musculu
    10    736.5   28.2    1184  1   FBL2_HUMAN            P98095 homo sapien
    11      722   27.7     704  1   FBL1_CHICK            O73775 gallus gall
    12      711   27.2     598  1   FBL1_CERAE            Q8mjj9 cercopithec
    13      695   26.6     703  1   FBL1_HUMAN            P23142 homo sapien
    14      685   26.2     705  1   FBL1_MOUSE            Q08879 mus musculu
    15    654.5   25.1     681  1   FBL1_BRARE            O42182 brachydanio
    16      573   22.0     798  1   FBL1_CAEEL            O77469 caenorhabdi
    17      537   20.6    1394  1   LTBS_HUMAN            P22064 homo sapien
```

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 31.4947 Seconds
                                            (without alignments)
                                            3777.210 Million cell updates/sec

Title: US-09-674-330A-8
Perfect score: 2610
Sequence: 1 MGPRSFEPMHSGLCRQRRMI..........INFRGSSVIRLRIYVSQYPF 461

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SPTREMBL_23:*
                1:   sp_archea:*
                2:   sp_bacteria:*
                3:   sp_fungi:*
                4:   sp_human:*
                5:   sp_invertebrate:*
                6:   sp_mammal:*
                7:   sp_mhc:*
                8:   sp_organelle:*
                9:   sp_phage:*
               10:   sp_plant:*
               11:   sp_rodent:*
               12:   sp_virus:*
               13:   sp_vertebrate:*
               14:   sp_unclassified:*
               15:   sp_rvirus:*
               16:   sp_bacteriap:*
               17:   sp_archeap:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1268	48.6	443	4	Q96TF5	Q96tf5 homo sapien
2	1258	48.2	443	11	Q9JM06	Q9jm06 mus musculu
3	1245	47.7	443	4	Q9H3D5	Q9h3d5 homo sapien
4	1109	42.5	493	11	Q8BPB5	Q8bpb5 mus musculu
5	967	37.0	387	11	Q8K0J4	Q8k0j4 mus musculu
6	767.5	29.4	1174	11	Q99K58	Q99k58 mus musculu
7	738.5	28.3	576	4	Q9Y3V7	Q9y3v7 homo sapien
8	737.5	28.3	1231	4	Q8IUI1	Q8iui1 homo sapien
9	736.5	28.2	1231	4	Q8IUI0	Q8iui0 homo sapien
10	730.5	28.0	685	11	Q922K8	Q922k8 mus musculu
11	730.5	28.0	685	11	Q8C3B1	Q8c3b1 mus musculu
12	729.5	28.0	683	4	Q8TBH8	Q8tbh8 homo sapien
13	722	27.7	704	13	O73774	O73774 gallus gall
14	711	27.2	598	6	Q8MJJ9	Q8mjj9 cercopithec
15	690	26.4	638	4	Q8NBH6	Q8nbh6 homo sapien
16	664.5	25.5	495	4	Q9HBQ5	Q9hbq5 homo sapien
17	654.5	25.1	681	13	O42182	O42182 brachydanio
18	620	23.8	698	5	Q9V4B8	Q9v4b8 drosophila
19	577.5	22.1	554	4	Q9UH16	Q9uh16 homo sapien
20	561	21.5	1409	5	Q9VS89	Q9vs89 drosophila
21	557	21.3	2673	4	Q96SC3	Q96sc3 homo sapien
22	546	20.9	5636	4	Q96RW7	Q96rw7 homo sapien
23	527.5	20.2	2872	11	Q9WUH8	Q9wuh8 rattus norv
24	527	20.2	3857	11	O88840	O88840 mus musculu
25	526.5	20.2	2809	4	Q96JP8	Q96jp8 homo sapien
26	524.5	20.1	1398	13	Q8AXM6	Q8axm6 xenopus lae
27	524.5	20.1	1399	13	Q8JFZ4	Q8jfz4 xenopus lae
28	520.5	19.9	741	4	Q96K89	Q96k89 homo sapien
29	515	19.7	1389	11	Q8CG18	Q8cg18 mus musculu
30	515	19.7	1713	11	Q8CG19	Q8cg19 mus musculu
31	514.5	19.7	2906	11	Q9WUH9	Q9wuh9 rattus norv
32	514	19.7	188	11	Q8R1U8	Q8r1u8 mus musculu
33	513	19.7	787	11	Q8K061	Q8k061 mus musculu
34	511	19.6	1713	11	O88349	O88349 mus musculu
35	509.5	19.5	708	13	P87363	P87363 gallus gall
36	503.5	19.3	937	5	Q9BLJ1	Q9blj1 ciona intes
37	496	19.0	729	11	Q8BNH3	Q8bnh3 mus musculu
38	495	19.0	1963	6	Q28019	Q28019 bos taurus
39	492.5	18.9	746	4	Q96HB9	Q96hb9 homo sapien
40	492.5	18.9	893	6	Q8MJK0	Q8mjk0 cercopithec
41	492.5	18.9	1256	4	Q9NS15	Q9ns15 homo sapien
42	492.5	18.9	1382	4	Q9H7K2	Q9h7k2 homo sapien
43	492	18.9	1289	5	Q8SSS3	Q8sss3 dictyosteli
44	492	18.9	1764	11	O35806	O35806 rattus norv
45	489.5	18.8	1062	11	Q60789	Q60789 mus musculu

ALIGNMENTS

RESULT 1
Q96TF5

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 33.9797 Seconds
                                        (without alignments)
                                        1975.923 Million cell updates/sec

Title: US-09-674-330A-9⟨
Perfect score: 2403
Sequence: 1 QCTNGFDLDRQSGQCLDIDE..........INFRGSSVIRLRIYVSQYPF 423

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_19Jun03:*
                1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
                2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
                3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
                4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
                5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
                6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
                7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
                8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
                9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
                10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
                11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
                12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
                13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
                14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
                15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
                16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
                17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
                18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
                19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
                20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
                21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
                22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
                23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
                24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2403	100.0	423	21	AAY56751	Smooth muscle prol
2	2403	100.0	423	21	AAY56753	Smooth muscle prol
3	2403	100.0	448	21	AAY56750	Smooth muscle prol
4	2403	100.0	448	21	AAY54990	Full length mouse
5	2403	100.0	461	21	AAY56752	Smooth muscle prol
6	2403	100.0	461	21	AAY54991	Full length mouse
7	2302	95.8	448	19	AAW79739 — *HUMAN*	Human EEGF protein
8	2302	95.8	448	20	AAW95709	Homo sapiens fetal
9	2302	95.8	448	20	AAW94281	Human extracellula
10	2302	95.8	448	21	AAY57058	Amino acid sequenc
11	2302	95.8	448	21	AAY54989	Full length human
12	2302	95.8	448	22	AAM93573	Human polypeptide,
13	2302	95.8	448	23	AAU75494	Human extracellula
14	2296	95.5	448	20	AAY08063 — *HUMAN*	Human EGF-like hom
15	2296	95.5	448	22	AAU29227	Human PRO polypept
16	2296	95.5	448	22	AAB31183	Amino acid sequenc
17	2296	95.5	448	24	ABU71315	Human PRO210 prote
18	2296	95.5	448	24	ABU72040	Novel human secret
19	2296	95.5	448	24	ABU65772	Human secreted/tra
20	2296	95.5	448	24	ABU66105	Novel human secret
21	2296	95.5	448	24	ABU67141	Novel human secret
22	2296	95.5	448	24	ABU67272	Novel human secret
23	2296	95.5	448	24	ABU67609	Human secreted/tra
24	2296	95.5	448	24	ABU65467	Human PRO polypept
25	2296	95.5	448	24	ABU58603	Human PRO polypept
26	2296	95.5	448	24	ABU56139	Human secreted/tra
27	2296	95.5	448	24	ABU57134	Human PRO polypept
28	2296	95.5	448	24	ABU10713	Human secreted/tra
29	2125	88.4	392	18	AAW31705	Human extracellula
30	1869	77.8	335	21	AAY76008	Rat EGF extracellu
31	1869	77.8	335	22	AAB55947	Skin cell protein,
32	1869	77.8	335	23	ABB72147	Rat protein isolat
33	1264.5	52.6	443	18	AAW32110	Human extracellula
34	1264.5	52.6	443	20	AAY16587	Extracellular prot
35	1264.5	52.6	443	21	AAB33418	Human PRO226 prote
36	1264.5	52.6	443	21	AAY84707	A human p53 mutant
37	1264.5	52.6	443	21	AAY55850	Human S1-5. ECMP-li
38	1264.5	52.6	443	22	AAU12330	Human PRO226 polyp
39	1264.5	52.6	443	23	AAU86130	Human PRO226 polyp
40	1264.5	52.6	443	24	ABU66728	Human PRO polypept
41	1264.5	52.6	443	24	ABU67004	Human secreted/tra
42	1264.5	52.6	443	24	ABU59809	Novel secreted and
43	1260.5	52.5	443	22	AAB92533	Human protein sequ
44	1252.5	52.1	443	21	AAY84706	Amino acid sequenc
45	1225.5	51.0	433	21	AAB58353	Lung cancer associ

Handwritten annotations: "94.8 % identical" bracketing results 7–13; "94.6 % identical" bracketing results 14–28.

ALIGNMENTS

```
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OM protein - protein search, using sw model

Run on:          December 12, 2003, 10:01:28 ; Search time 14.2905 Seconds
                                             (without alignments)
                                             1252.401 Million cell updates/sec


Title:           US-09-674-330A-9
Perfect score:   2403
Sequence:        1 QCTNGFDLDRQSGQCLDIDE..........INFRGSSVIRLRIYVSQYPF 423


Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5


Searched:        328717 seqs, 42310858 residues


Total number of hits satisfying chosen parameters:      328717


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :       Issued_Patents_AA:*
                 1:  /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                 2:  /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                 3:  /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                 4:  /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                 5:  /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 6:  /cgn2_6/ptodata/1/iaa/backfiles1.pep:*


     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                  SUMMARIES
                       %
     Result          .Query
       No.    Score  Match Length DB  ID                           Description
     ----------------------------------------------------------------------------
        1     2302    95.8    448  2   US-08-884-072-1 ⟩ human      Sequence 1, Appli
        2     2302    95.8    448  4   US-09-212-168-1 ⟋            Sequence 1, Appli
        3     1869    77.8    335  4   US-09-312-283C-186           Sequence 186, App
        4     1832    76.2    337  3   US-09-188-930-186            Sequence 186, App
        5    1264.5   52.6    443  2   US-08-833-963C-2             Sequence 2, Appli
        6    1264.5   52.6    443  3   US-08-980-514-1              Sequence 1, Appli
        7     966.5   40.2    387  2   US-08-884-072-5              Sequence 5, Appli
        8     966.5   40.2    387  2   US-08-833-963C-9             Sequence 9, Appli
        9     966.5   40.2    387  3   US-08-980-514-3              Sequence 3, Appli
       10     966.5   40.2    387  4   US-09-212-168-5              Sequence 5, Appli
       11     897.5   37.3    274  3   US-09-188-930-336            Sequence 336, App
```

94.8%

```
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OM protein - protein search, using sw model

Run on:          December 12, 2003, 10:05:03 ; Search time 24.7703 Seconds
                                            (without alignments)
                                            3176.029 Million cell updates/sec


Title:           US-09-674-330A-9
Perfect score:  2403
Sequence:        1 QCTNGFDLDRQSGQCLDIDE..........INFRGSSVIRLRIYVSQYPF 423


Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5


Searched:        684280 seqs, 185983659 residues


Total number of hits satisfying chosen parameters:      684280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :       Published_Applications_AA:*
                 1:  /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                 2:  /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                 3:  /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                 4:  /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
                 5:  /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                 6:  /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
                 7:  /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                 8:  /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                 9:  /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
                 10:  /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
                 11:  /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
                 12:  /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                 13:  /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                 14:  /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                 15:  /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
                 16:  /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                 17:  /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
                 18:  /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*


     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
```

```
                             SUMMARIES
                        %
 Result            Query
    No.    Score   Match  Length  DB  ID                           Description
    --------------------------------------------------------------------------------
       1    2302    95.8     448   9  US-09-083-002-2              Sequence 2, Appli
       2    2302    95.8     448   9  US-09-275-805-2              Sequence 2, Appli
       3    2302    95.8     448   9  US-09-836-561-1              Sequence 1, Appli
       4    2302    95.8     448  14  US-10-041-016-2              Sequence 2, Appli
       5    2296    95.5     448  12  US-10-199-672-408            Sequence 408, App
       6    2296    95.5     448  12  US-10-187-749-408            Sequence 408, App
       7    2296    95.5     448  12  US-10-194-457-408            Sequence 408, App
       8    2296    95.5     448  12  US-10-184-642-408            Sequence 408, App
       9    2296    95.5     448  12  US-10-196-747-408            Sequence 408, App
      10    2296    95.5     448  12  US-10-173-689-408            Sequence 408, App
      11    2296    95.5     448  12  US-10-173-690-408            Sequence 408, App
      12    2296    95.5     448  12  US-10-173-691-408            Sequence 408, App
      13    2296    95.5     448  12  US-10-173-692-408            Sequence 408, App
      14    2296    95.5     448  12  US-10-173-694-408            Sequence 408, App
      15    2296    95.5     448  12  US-10-173-698-408            Sequence 408, App
      16    2296    95.5     448  12  US-10-173-699-408            Sequence 408, App
      17    2296    95.5     448  12  US-10-173-707-408            Sequence 408, App
      18    2296    95.5     448  12  US-10-174-569-408            Sequence 408, App
      19    2296    95.5     448  12  US-10-174-583-408            Sequence 408, App
      20    2296    95.5     448  12  US-10-174-587-408            Sequence 408, App
      21    2296    95.5     448  12  US-10-174-589-408            Sequence 408, App
      22    2296    95.5     448  12  US-10-174-591-408            Sequence 408, App
      23    2296    95.5     448  12  US-10-175-736-408            Sequence 408, App
      24    2296    95.5     448  12  US-10-175-742-408            Sequence 408, App
      25    2296    95.5     448  12  US-10-175-744-408            Sequence 408, App
      26    2296    95.5     448  12  US-10-175-745-408            Sequence 408, App
      27    2296    95.5     448  12  US-10-175-748-408            Sequence 408, App
      28    2296    95.5     448  12  US-10-175-751-408            Sequence 408, App
      29    2296    95.5     448  12  US-10-175-754-408            Sequence 408, App
      30    2296    95.5     448  12  US-10-176-480-408            Sequence 408, App
      31    2296    95.5     448  12  US-10-176-489-408            Sequence 408, App
      32    2296    95.5     448  12  US-10-176-754-408            Sequence 408, App
      33    2296    95.5     448  12  US-10-176-755-408            Sequence 408, App
      34    2296    95.5     448  12  US-10-176-759-408            Sequence 408, App
      35    2296    95.5     448  12  US-10-176-920-408            Sequence 408, App
      36    2296    95.5     448  12  US-10-176-922-408            Sequence 408, App
      37    2296    95.5     448  12  US-10-176-924-408            Sequence 408, App
      38    2296    95.5     448  12  US-10-176-984-408            Sequence 408, App
      39    2296    95.5     448  12  US-10-179-508-408            Sequence 408, App
      40    2296    95.5     448  12  US-10-179-512-408            Sequence 408, App
      41    2296    95.5     448  12  US-10-179-515-408            Sequence 408, App
      42    2296    95.5     448  12  US-10-066-198-15             Sequence 15, Appl
      43    2296    95.5     448  12  US-10-173-702-408            Sequence 408, App
      44    2296    95.5     448  12  US-10-173-703-408            Sequence 408, App
      45    2296    95.5     448  12  US-10-173-704-408            Sequence 408, App


                             ALIGNMENTS



RESULT 1
US-09-083-002-2
```

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 13.3378 Seconds
                                              (without alignments)
                                              3049.921 Million cell updates/sec

Title: US-09-674-330A-9
Perfect score: 2403
Sequence: 1 QCTNGFDLDRQSGQCLDIDE..........INFRGSSVIRLRIYVSQYPF 423

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_76:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                  SUMMARIES
                        %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
      1 1118.5   46.5   493 2   JC5621   epidermal growth f
      2   966.5   40.2   387 2   I38449   extracellular prot
      3   754.5   31.4   1221 2   A49457   fibulin-2 precurso
      4   733.5   30.5   685 2   S78040   fibulin, splice fo
      5   729.5   30.4   683 2   C36346   fibulin 1 precurso
      6   726.5   30.2   1184 2   A55184   fibulin-2 precurso
      7   688   28.6   705 2   S34968   fibulin, splice fo
      8   613.5   25.5   601 2   B36346   fibulin 1 precurso
      9   608   25.3   689 2   T42760   fibulin, splice fo
     10   600   25.0   712 2   T42990   fibulin 1, splice
     11   597.5   24.9   589 2   T43210   fibulin-1D precurs
     12   573   23.8   798 2   T22793   hypothetical prote
     13   537   22.3   1394 2   A35626   transforming growt

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 8.57432 Seconds
                                              (without alignments)
                                              2319.984 Million cell updates/sec

Title: US-09-674-330A-9
Perfect score: 2403
Sequence: 1 QCTNGFDLDRQSGQCLDIDE..........INFRGSSVIRLRIYVSQYPF 423

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SwissProt_41:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
  No.   Score Match Length DB ID   Description
----
    1   2403 100.0   448 1   FBL5_MOUSE   Nakamura Q9wvh9 mus musculu
    2   2367   98.5   448 1   FBL5_RAT   at al. LATE Q9wvh8 rattus norv
    3   2302   95.8   448 1   FBL5_HUMAN   Q9ubx5 homo sapien
    4 1264.5   52.6   443 1   FBL4_HUMAN   O95967 homo sapien
    5 1257.5   52.3   443 1   FBL4_CRIGR   O55058 cricetulus
    6 1252.5   52.1   443 1   FBL4_MOUSE   Q9wvj9 mus musculu
    7 1118.5   46.5   493 1   FBL3_RAT   O35568 rattus norv
    8 1098.5   45.7   493 1   FBL3_HUMAN   Q12805 homo sapien
    9   754.5   31.4   1221 1   FBL2_MOUSE   P37889 mus musculu
   10   726.5   30.2   1184 1   FBL2_HUMAN   P98095 homo sapien
   11   722   30.0   704 1   FBL1_CHICK   O73775 gallus gall
   12   711   29.6   598 1   FBL1_CERAE   Q8mjj9 cercopithec
   13   695   28.9   703 1   FBL1_HUMAN   P23142 homo sapien
   14   685   28.5   705 1   FBL1_MOUSE   Q08879 mus musculu
   15   653.5   27.2   681 1   FBL1_BRARE   O42182 brachydanio
   16   573   23.8   798 1   FBL1_CAEEL   O77469 caenorhabdi
   17   537   22.3   1394 1   LTBS_HUMAN   P22064 homo sapien

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OM protein - protein search, using sw model

Run on: December 12, 2003, 10:00:22 ; Search time 28.8986 Seconds
                                        (without alignments)
                                        3777.210 Million cell updates/sec

Title: US-09-674-330A-9
Perfect score: 2403
Sequence: 1 QCTNGFDLDRQSGQCLDIDE..........INFRGSSVIRLRIYVSQYPF 423

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SPTREMBL_23:*
           1:   sp_archea:*
           2:   sp_bacteria:*
           3:   sp_fungi:*
           4:   sp_human:*
           5:   sp_invertebrate:*
           6:   sp_mammal:*
           7:   sp_mhc:*
           8:   sp_organelle:*
           9:   sp_phage:*
          10:   sp_plant:*
          11:   sp_rodent:*
          12:   sp_virus:*
          13:   sp_vertebrate:*
          14:   sp_unclassified:*
          15:   sp_rvirus:*
          16:   sp_bacteriap:*
          17:   sp_archeap:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1264.5	52.6	443	4	Q96TF5	Q96tf5 homo sapien
2	1253.5	52.2	443	11	Q9JM06	Q9jm06 mus musculu
3	1241.5	51.7	443	4	Q9H3D5	Q9h3d5 homo sapien
4	1107.5	46.1	493	11	Q8BPB5	Q8bpb5 mus musculu
5	967	40.2	387	11	Q8K0J4	Q8k0j4 mus musculu
6	757.5	31.5	1174	11	Q99K58	Q99k58 mus musculu
7	730.5	30.4	685	11	Q922K8	Q922k8 mus musculu
8	730.5	30.4	685	11	Q8C3B1	Q8c3b1 mus musculu
9	729.5	30.4	683	4	Q8TBH8	Q8tbh8 homo sapien
10	728.5	30.3	576	4	Q9Y3V7	Q9y3v7 homo sapien
11	727.5	30.3	1231	4	Q8IUI1	Q8iui1 homo sapien
12	726.5	30.2	1231	4	Q8IUI0	Q8iui0 homo sapien
13	722	30.0	704	13	O73774	O73774 gallus gall
14	711	29.6	598	6	Q8MJJ9	Q8mjj9 cercopithec
15	690	28.7	638	4	Q8NBH6	Q8nbh6 homo sapien
16	664.5	27.7	495	4	Q9HBQ5	Q9hbq5 homo sapien
17	653.5	27.2	681	13	O42182	O42182 brachydanio
18	615	25.6	698	5	Q9V4B8	Q9v4b8 drosophila
19	577.5	24.0	554	4	Q9UH16	Q9uh16 homo sapien
20	557	23.2	2673	4	Q96SC3	Q96sc3 homo sapien
21	554.5	23.1	1409	5	Q9VS89	Q9vs89 drosophila
22	546	22.7	5636	4	Q96RW7	Q96rw7 homo sapien
23	524.5	21.8	1398	13	Q8AXM6	Q8axm6 xenopus lae
24	524.5	21.8	1399	13	Q8JFZ4	Q8jfz4 xenopus lae
25	524.5	21.8	2872	11	Q9WUH8	Q9wuh8 rattus norv
26	524	21.8	3857	11	O88840	O88840 mus musculu
27	523.5	21.8	2809	4	Q96JP8	Q96jp8 homo sapien
28	515.5	21.5	741	4	Q96K89	Q96k89 homo sapien
29	515	21.4	1389	11	Q8CG18	Q8cg18 mus musculu
30	515	21.4	1713	11	Q8CG19	Q8cg19 mus musculu
31	514	21.4	188	11	Q8R1U8	Q8r1u8 mus musculu
32	511	21.3	1713	11	O88349	O88349 mus musculu
33	510.5	21.2	2906	11	Q9WUH9	Q9wuh9 rattus norv
34	506.5	21.1	708	13	P87363	P87363 gallus gall
35	504	21.0	787	11	Q8K061	Q8k061 mus musculu
36	495.5	20.6	937	5	Q9BLJ1	Q9blj1 ciona intes
37	490	20.4	1963	6	Q28019	Q28019 bos taurus
38	486.5	20.2	729	11	Q8BNH3	Q8bnh3 mus musculu
39	485.5	20.2	746	4	Q96HB9	Q96hb9 homo sapien
40	485.5	20.2	893	6	Q8MJK0	Q8mjk0 cercopithec
41	485.5	20.2	1256	4	Q9NS15	Q9ns15 homo sapien
42	485.5	20.2	1382	4	Q9H7K2	Q9h7k2 homo sapien
43	484.5	20.2	517	4	Q9NP01	Q9np01 homo sapien
44	483.5	20.1	1764	11	O35806	O35806 rattus norv
45	482	20.1	1289	5	Q8SSS3	Q8sss3 dictyosteli

ALIGNMENTS

RESULT 1
Q96TF5

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 07:36:19 ; Search time 4857.03 Seconds
                                     (without alignments)
                                     11320.190 Million cell updates/sec

Title: US-09-674-330A-1
Perfect score: 1344
Sequence: 1 atgccaggattaaaaaggat..........atgtgtcgcagtatccgttc 1344

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
             1:   gb_ba:*
             2:   gb_htg:*
             3:   gb_in:*
             4:   gb_om:*
             5:   gb_ov:*
             6:   gb_pat:*
             7:   gb_ph:*
             8:   gb_pl:*
             9:   gb_pr:*
            10:   gb_ro:*
            11:   gb_sts:*
            12:   gb_sy:*
            13:   gb_un:*
            14:   gb_vi:*
            15:   em_ba:*
            16:   em_fun:*
            17:   em_hum:*
            18:   em_in:*
            19:   em_mu:*
            20:   em_om:*
            21:   em_or:*
            22:   em_ov:*
            23:   em_pat:*
            24:   em_ph:*
            25:   em_pl:*
            26:   em_ro:*
            27:   em_sts:*

```
              28:   em_un:*
              29:   em_vi:*
              30:   em_htg_hum:*
              31:   em_htg_inv:*
              32:   em_htg_other:*
              33:   em_htg_mus:*
              34:   em_htg_pln:*
              35:   em_htg_rod:*
              36:   em_htg_mam:*
              37:   em_htg_vrt:*  .
              38:   em_sy:*
              39:   em_htgo_hum:*
              40:   em_htgo_mus:*
              41:   em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

<div align="center">SUMMARIES</div>

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1344	100.0	2230	10	BC006636	BC006636 Mus muscu
2	1344	100.0	2478	10	AF112151	AF112151 Mus muscu
3	1233.6	91.8	2499	10	AF112153	AF112153 Rattus no
4	1232	91.7	2304	10	AF137350	AF137350 Rattus no
5	1113.6	82.9	1720	6	A84086	A84086 Sequence 1
6	1113.6	82.9	2019	9	HSA133490	AJ133490 Homo sapi
7	1113.6	82.9	2126	6	BD127534	BD127534 Primer fo
8	1113.6	82.9	2126	9	AK075147	AK075147 Homo sapi
9	1113.6	82.9	2328	9	AF112152	AF112152 Homo sapi
10	1113.6	82.9	2367	9	BC022280	BC022280 Homo sapi
11	1113.6	82.9	2550	6	AR036548	AR036548 Sequence
12	1113.6	82.9	2550	6	AR173204	AR173204 Sequence
13	1113.6	82.9	2550	6	BD132822	BD132822 human ext
14	1112	82.7	2609	6	AX376340	AX376340 Sequence
15	1112	82.7	2609	6	AX403659	AX403659 Sequence
16	1097.6	81.7	2019	9	AF093118	AF093118 Homo sapi
17	604.6	45.0	853	6	BD124625	BD124625 Primer fo
18	604.6	45.0	853	6	BD126198	BD126198 Primer fo
19	604.6	45.0	1538	6	BD127158	BD127158 Primer fo
20	604.6	45.0	1538	9	AK074540	AK074540 Homo sapi
21	350.8	26.1	1440	9	HSA132819	AJ132819 Homo sapi
22	350.8	26.1	1536	9	AB030655	AB030655 Homo sapi
23	350.4	26.1	1707	6	BD155763	BD155763 Primer fo
24	350.4	26.1	1707	9	AK000980	AK000980 Homo sapi
25	349.2	26.0	1480	6	AX023967	AX023967 Sequence
26	349.2	26.0	1561	9	BC010456	BC010456 Homo sapi
27	349.2	26.0	1866	9	AK075453	AK075453 Homo sapi
28	347.6	25.9	1757	6	AX577988	AX577988 Sequence
29	347.6	25.9	1757	9	AF109121	AF109121 Homo sapi
30	347.6	25.9	1875	6	AX201326	AX201326 Sequence
31	347.6	25.9	1875	6	AX464184	AX464184 Sequence
32	347.6	25.9	2018	6	AR095382	AR095382 Sequence
33	344.4	25.6	1778	10	AF046870	AF046870 Cricetulu

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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 21:43:31 ; Search time 343.399 Seconds
                                              (without alignments)
                                              10565.088 Million cell updates/sec

Title: US-09-674-330A-1
Perfect score: 1344
Sequence: 1 atgccaggattaaaaaggat..........atgtgtcgcagtatccgttc 1344

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_19Jun03:*
                   1:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980..DAT:*
                   2:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
                   3:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
                   4:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
                   5:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
                   6:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
                   7:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
                   8:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
                   9:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
                   10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
                   11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
                   12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
                   13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
                   14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
                   15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
                   16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
                   17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
                   18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
                   19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
                   20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
                   21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
                   22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
                   23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
                   24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
                   25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

      Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1344	100.0	1344	21	AAZ39383	Smooth muscle prol
2	1344	100.0	2233	21	AAZ39384	Smooth muscle prol
3	1344	100.0	2233	21	AAZ40029	Full length mouse
4	1327.4	98.8	1383	21	AAZ39386	Smooth muscle prol
5	1327.4	98.8	2429	21	AAZ39387	Smooth muscle prol
6	1327.4	98.8	2429	21	AAZ40031	Full length mouse
7	1269	94.4	1269	21	AAZ39385	Smooth muscle prol
8	1269	94.4	1269	21	AAZ39388	Smooth muscle prol
9	1113.6	82.9	1347	24	ABL52528	Human UP50 cDNA se
10	1113.6	82.9	1720	19	AAV62432	Human EEGF genomic
11	1113.6	82.9	1720	24	ABK13627	Human cDNA encodin
12	1113.6	82.9	2126	22	AAK94505	Human full-length
13	1113.6	82.9	2328	21	AAZ40027	Full length human
14	1113.6	82.9	2362	20	AAX07567	Homo sapiens fetal
15	1113.6	82.9	2362	21	AAZ39892	cDNA sequence of t
16	1113.6	82.9	2550	20	AAX05359	Human extracellula
17	1112	82.7	2509	20	AAX37670	Human EGF-like hom
18	1112	82.7	2609	22	AAS46128	Human DNA encoding
19	1112	82.7	2609	22	AAC86968	Nucleotide sequenc
20	1112	82.7	2609	25	ACA57886	Human PRO210 cDNA.
21	1112	82.7	2609	25	ACA60458	Novel human secret
22	1112	82.7	2609	25	ABX98356	Human cDNA encodin
23	1112	82.7	2609	25	ABX98858	Novel human secret
24	1112	82.7	2609	25	ACA04448	Novel human secret
25	1112	82.7	2609	25	ACA04928	Novel human secret
26	1112	82.7	2609	25	ACA05903	Human secreted/tra
27	1112	82.7	2609	25	ABX97947	Human PRO polynucl
28	1112	82.7	2609	25	ABX78731	Human PRO polynucl
29	1112	82.7	2609	25	ABX75744	Human cDNA encodin
30	1112	82.7	2609	25	ABX76949	Human PRO polynucl
31	1112	82.7	2609	25	ABX16789	Human cDNA encodin
32	1097.6	81.7	2019	24	ABT10172	Human breast cance
33	1000.8	74.5	1228	18	AAT89380	Human extracellula
34	922.2	68.6	1254	21	AAZ61672	cDNA encoding rat
35	922.2	68.6	1254	22	AAC99605	Skin cell cDNA, SE
36	920.2	68.5	1260	24	ABL34757	Rat cDNA isolated
37	650	48.4	778	20	AAX37673	Human PRO protein
38	604.6	45.0	853	22	AAK91596	Human cDNA 5'-end
39	604.6	45.0	853	22	AAK93169	Human cDNA clone r
40	604.6	45.0	1538	22	AAK94129	Human full-length
41	516	38.4	680	21	AAA44245	Human secreted exp
42	350.4	26.1	1707	22	AAH13771	Human cDNA sequenc
43	349.2	26.0	1480	21	AAA14608	cDNA encoding a hu
44	349.2	26.0	1525	18	AAT88974	Human extracellula
45	349.2	26.0	1531	20	AAX60351	Extracellular prot

ALIGNMENTS

```
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OM nucleic - nucleic search, using sw model

Run on:          December 13, 2003, 12:56:44 ; Search time 90.1381 Seconds
                                             (without alignments)
                                             6581.220 Million cell updates/sec


Title:           US-09-674-330A-1
Perfect score:   1344
Sequence:        1 atgccaggattaaaaaggat.........atgtgtcgcagtatccgttc 1344


Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0


Searched:        569978 seqs, 220691566 residues


Total number of hits satisfying chosen parameters:      1139956


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :       Issued_Patents_NA:*
                 1:  /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                 2:  /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                 3:  /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                 4:  /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                 5:  /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 6:  /cgn2_6/ptodata/2/ina/backfiles1.seq:*


     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.


                              SUMMARIES
                       %
Result             Query
   No.    Score   Match Length DB   ID                        Description
-----------------------------------------------------------------------------
     1   1113.6    82.9   2550  2   US-08-884-072-2           Sequence 2, Appli
     2   1113.6    82.9   2550  4   US-09-212-168-2           Sequence 2, Appli
     3    922.2    68.6   1254  4   US-09-312-283C-67         Sequence 67, Appl
     4    920.2    68.5   1260  3   US-09-188-930-67          Sequence 67, Appl
     5    349.2    26.0   1531  2   US-08-833-963C-1          Sequence 1, Appli
     6    347.6    25.9   2018  3   US-08-980-514-2           Sequence 2, Appli
     7    289.4    21.5   1018  3   US-09-188-930-259         Sequence 259, App
     8    289.4    21.5   1018  4   US-09-312-283C-259        Sequence 259, App
     9    244.6    18.2   2512  4   US-09-248-757-1           Sequence 1, Appli
    10    102.8     7.6   3373  2   US-08-897-443-2           Sequence 2, Appli
    11     92.4     6.9    401  4   US-09-643-597-278         Sequence 278, App
```

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 18:05:35 ; Search time 424.12 Seconds
                                         (without alignments)
                                         10532.199 Million cell updates/sec

Title: US-09-674-330A-1
Perfect score: 1344
Sequence: 1 atgccaggattaaaaaggat.........atgtgtcgcagtatccgttc 1344

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
          1:   /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
          2:   /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
          3:   /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
          4:   /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
          5:   /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
          6:   /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
          7:   /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
          8:   /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
          9:   /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
          10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
          11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
          12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
          13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
          14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
          15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
          16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
          17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
          18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

```
                                    SUMMARIES
                            %
Result               Query
    No.     Score   Match  Length  DB   ID                              Description
--------------------------------------------------------------------------------------------
      1    1233.6   91.8    2499   15   US-10-175-523-164               Sequence 164, App
      2    1113.6   82.9    1717    9   US-09-275-805-1                 Sequence 1, Appli
      3    1113.6   82.9    2362    9   US-09-083-002-1                 Sequence 1, Appli
      4    1113.6   82.9    2362   14   US-10-041-016-1                 Sequence 1, Appli
      5    1113.6   82.9    2550    9   US-09-836-561-2                 Sequence 2, Appli
      6    1112     82.7    2609   13   US-10-199-672-407               Sequence 407, App
      7    1112     82.7    2609   13   US-10-187-749-407               Sequence 407, App
      8    1112     82.7    2609   13   US-10-194-457-407               Sequence 407, App
      9    1112     82.7    2609   13   US-10-184-642-407               Sequence 407, App
     10    1112     82.7    2609   13   US-10-196-747-407               Sequence 407, App
     11    1112     82.7    2609   13   US-10-173-689-407               Sequence 407, App
     12    1112     82.7    2609   13   US-10-173-690-407               Sequence 407, App
     13    1112     82.7    2609   13   US-10-173-691-407               Sequence 407, App
     14    1112     82.7    2609   13   US-10-173-692-407               Sequence 407, App
     15    1112     82.7    2609   13   US-10-173-694-407               Sequence 407, App
     16    1112     82.7    2609   13   US-10-173-698-407               Sequence 407, App
     17    1112     82.7    2609   13   US-10-173-699-407               Sequence 407, App
     18    1112     82.7    2609   13   US-10-173-707-407               Sequence 407, App
     19    1112     82.7    2609   13   US-10-174-569-407               Sequence 407, App
     20    1112     82.7    2609   13   US-10-174-583-407               Sequence 407, App
     21    1112     82.7    2609   13   US-10-174-587-407               Sequence 407, App
     22    1112     82.7    2609   13   US-10-174-589-407               Sequence 407, App
     23    1112     82.7    2609   13   US-10-174-591-407               Sequence 407, App
     24    1112     82.7    2609   13   US-10-175-736-407               Sequence 407, App
     25    1112     82.7    2609   13   US-10-175-742-407               Sequence 407, App
     26    1112     82.7    2609   13   US-10-175-744-407               Sequence 407, App
     27    1112     82.7    2609   13   US-10-175-745-407               Sequence 407, App
     28    1112     82.7    2609   13   US-10-175-748-407               Sequence 407, App
     29    1112     82.7    2609   13   US-10-175-751-407               Sequence 407, App
     30    1112     82.7    2609   13   US-10-175-754-407               Sequence 407, App
     31    1112     82.7    2609   13   US-10-176-480-407               Sequence 407, App
     32    1112     82.7    2609   13   US-10-176-489-407               Sequence 407, App
     33    1112     82.7    2609   13   US-10-176-754-407               Sequence 407, App
     34    1112     82.7    2609   13   US-10-176-755-407               Sequence 407, App
     35    1112     82.7    2609   13   US-10-176-759-407               Sequence 407, App
     36    1112     82.7    2609   13   US-10-176-920-407               Sequence 407, App
     37    1112     82.7    2609   13   US-10-176-922-407               Sequence 407, App
     38    1112     82.7    2609   13   US-10-176-924-407               Sequence 407, App
     39    1112     82.7    2609   13   US-10-176-984-407               Sequence 407, App
     40    1112     82.7    2609   13   US-10-179-508-407               Sequence 407, App
     41    1112     82.7    2609   13   US-10-179-512-407               Sequence 407, App
     42    1112     82.7    2609   13   US-10-179-515-407               Sequence 407, App
     43    1112     82.7    2609   13   US-10-066-198-14                Sequence 14, Appl
     44    1112     82.7    2609   13   US-10-173-702-407               Sequence 407, App
     45    1112     82.7    2609   13   US-10-173-703-407               Sequence 407, App


                                    ALIGNMENTS


RESULT 1
US-10-175-523-164
```

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 12:45:39 ; Search time 2631.5 Seconds
                                              (without alignments)
                                              12413.176 Million cell updates/sec

Title: US-09-674-330A-1
Perfect score: 1344
Sequence: 1 atgccaggattaaaaaggat..........atgtgtcgcagtatccgttc 1344

Scoring table: IDENTITY_NUC
                    Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                    1:   em_estba:*
                    2:   em_esthum:*
                    3:   em_estin:*
                    4:   em_estmu:*
                    5:   em_estov:*
                    6:   em_estpl:*
                    7:   em_estro:*
                    8:   em_htc:*
                    9:   gb_est1:*
                    10: gb_est2:*
                    11: gb_htc:*
                    12: gb_est3:*
                    13: gb_est4:*
                    14: gb_est5:*
                    15: em_estfun:*
                    16: em_estom:*
                    17: em_gss_hum:*
                    18: em_gss_inv:*
                    19: em_gss_pln:*
                    20: em_gss_vrt:*
                    21: em_gss_fun:*
                    22: em_gss_mam:*
                    23: em_gss_mus:*
                    24: em_gss_pro:*
                    25: em_gss_rod:*
                    26: em_gss_phg:*
                    27: em_gss_vrl:*

```
                28:  gb_gss1:*
                29:  gb_gss2:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                     SUMMARIES
                      %
  Result          Query
     No.    Score  Match Length DB  ID                   Description
  ------------------------------------------------------------------------------
       1    1344   100.0   1835  11  AK085170             AK085170 Mus muscu
       2    1344   100.0   5831  11  AK090129             AK090129 Mus muscu
       3  1017.2    75.7   2423  11  CNSLT1I9S            BX248290 human ful
       4     771    57.4    980  13  BU520272             BU520272 AGENCOURT
       5   761.8    56.7    870  13  BQ930927             BQ930927 AGENCOURT
       6   760.8    56.6    796  12  BI453348             BI453348 603173067
       7   741.2    55.1   1796  11  AK084895             AK084895 Mus muscu
       8     731    54.4   1201  13  BX439363             BX439363 BX439363
       9     708    52.7    717  12  BI251219             BI251219 602994427
      10   706.4    52.6   1014  12  BM921371             BM921371 AGENCOURT
      11     706    52.5    912  13  BU149085             BU149085 AGENCOURT
      12   682.8    50.8    815  10  BG174360             BG174360 602336371
      13     679    50.5    877  13  BX326257             BX326257 BX326257
      14   678.2    50.5    842  13  BX367825             BX367825 BX367825
      15   672.8    50.1    996  13  BQ720516             BQ720516 AGENCOURT
      16   660.8    49.2    888  13  BX346924             BX346924 BX346924
      17   655.8    48.8    841  14  CD172152             CD172152 AGENCOURT
      18   649.4    48.3    954  12  BM545444             BM545444 AGENCOURT
      19   643.4    47.9    904  13  BQ716569             BQ716569 AGENCOURT
      20   642.6    47.8    952  13  BU148724             BU148724 AGENCOURT
      21   641.6    47.7    930  13  BX349066             BX349066 BX349066
      22   636.6    47.4    854  13  BX347366             BX347366 BX347366
  c   23   634.8    47.2    870  13  BX429526             BX429526 BX429526
      24     600    44.6    762  14  CB595725             CB595725 AGENCOURT
  c   25   580.4    43.2    923  13  BX326104             BX326104 BX326104
  c   26   580.2    43.2    954  13  BX371974             BX371974 BX371974
      27   562.4    41.8    654  14  CB595181             CB595181 AGENCOURT
  c   28   557.4    41.5    906  13  BX388741             BX388741 BX388741
      29   557.2    41.5    914  13  BX450129             BX450129 BX450129
      30     556    41.4    822  10  BG109391             BG109391 602280448
      31   550.6    41.0    891  10  BF339448             BF339448 602039102
      32   538.8    40.1    867  13  BX326018             BX326018 BX326018
      33     535    39.8    778  13  BU750981             BU750981 CH3#037_B
      34   531.2    39.5    894  13  BX408562             BX408562 BX408562
      35   530.4    39.5    644  12  BG938621             BG938621 cn27c11.x
      36     518    38.5    882  12  BI825121             BI825121 603038662
      37   502.6    37.4    835  13  BQ718885             BQ718885 AGENCOURT
      38   498.8    37.1   1101  10  BG245848             BG245848 602358649
      39     497    37.0    880  12  BI764020             BI764020 603043221
      40   489.4    36.4    680   9  AW106432             AW106432 um27g01.y
      41   486.2    36.2    636  14  BY753400             BY753400 BY753400
      42   482.2    35.9    627  12  BI183862             BI183862 UNL-P-FN-
  c   43   481.4    35.8    627  10  BF090699             BF090699 QV2-NT004
      44   472.4    35.1    933  13  BQ716088             BQ716088 AGENCOURT
      45     470    35.0    912  12  BI768516             BI768516 603057118
```

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 07:36:19 ; Search time 4997.97 Seconds
                                              (without alignments)
                                              11320.190 Million cell updates/sec

Title: US-09-674-330A-6
Perfect score: 1383
Sequence: 1 atgggacctagaagtttcga..........atgtgtcgcagtatccgttc 1383

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*
                 15: em_ba:*
                 16: em_fun:*
                 17: em_hum:*
                 18: em_in:*
                 19: em_mu:*
                 20: em_om:*
                 21: em_or:*
                 22: em_ov:*
                 23: em_pat:*
                 24: em_ph:*
                 25: em_pl:*
                 26: em_ro:*
                 27: em_sts:*

```
28:  em_un:*
29:  em_vi:*
30:  em_htg_hum:*
31:  em_htg_inv:*
32:  em_htg_other:*
33:  em_htg_mus:*
34:  em_htg_pln:*
35:  em_htg_rod:*
36:  em_htg_mam:*
37:  em_htg_vrt:*
38:  em_sy:*
39:  em_htgo_hum:*
40:  em_htgo_mus:*
41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1327.4	96.0	2230	10	BC006636	BC006636 Mus muscu
2	1327.4	96.0	2478	10	AF112151	AF112151 Mus muscu
3	1217	88.0	2499	10	AF112153	AF112153 Rattus no
4	1215.4	87.9	2304	10	AF137350	AF137350 Rattus no
5	1098.6	79.4	1720	6	A84086	A84086 Sequence 1
6	1098.6	79.4	2019	9	HSA133490	AJ133490 Homo sapi
7	1098.6	79.4	2126	6	BD127534	BD127534 Primer fo
8	1098.6	79.4	2126	9	AK075147	AK075147 Homo sapi
9	1098.6	79.4	2328	9	AF112152	AF112152 Homo sapi
10	1098.6	79.4	2367	9	BC022280	BC022280 Homo sapi
11	1098.6	79.4	2550	6	AR036548	AR036548 Sequence
12	1098.6	79.4	2550	6	AR173204	AR173204 Sequence
13	1098.6	79.4	2550	6	BD132822	BD132822 human ext
14	1097	79.3	2609	6	AX376340	AX376340 Sequence
15	1097	79.3	2609	6	AX403659	AX403659 Sequence
16	1082.6	78.3	2019	9	AF093118	AF093118 Homo sapi
17	604.6	43.7	853	6	BD124625	BD124625 Primer fo
18	604.6	43.7	853	6	BD126198	BD126198 Primer fo
19	604.6	43.7	1538	6	BD127158	BD127158 Primer fo
20	604.6	43.7	1538	9	AK074540	AK074540 Homo sapi
21	350.8	25.4	1440	9	HSA132819	AJ132819 Homo sapi
22	350.8	25.4	1536	9	AB030655	AB030655 Homo sapi
23	350.4	25.3	1707	6	BD155763	BD155763 Primer fo
24	350.4	25.3	1707	9	AK000980	AK000980 Homo sapi
25	349.2	25.2	1480	6	AX023967	AX023967 Sequence
26	349.2	25.2	1561	9	BC010456	BC010456 Homo sapi
27	349.2	25.2	1866	9	AK075453	AK075453 Homo sapi
28	347.6	25.1	1757	6	AX577988	AX577988 Sequence
29	347.6	25.1	1757	9	AF109121	AF109121 Homo sapi
30	347.6	25.1	1875	6	AX201326	AX201326 Sequence
31	347.6	25.1	1875	6	AX464184	AX464184 Sequence
32	347.6	25.1	2018	6	AR095382	AR095382 Sequence
33	344.4	24.9	1778	10	AF046870	AF046870 Cricetulu

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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 21:43:31 ; Search time 353.364 Seconds
                                             (without alignments)
                                             10565.088 Million cell updates/sec

Title: US-09-674-330A-6
Perfect score: 1383
Sequence: 1 atgggacctagaagtttcga..........atgtgtcgcagtatccgttc 1383

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_19Jun03:*
                 1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
                 2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
                 3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
                 4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
                 5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
                 6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
                 7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
                 8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
                 9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
                 10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
                 11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
                 12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
                 13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
                 14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
                 15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
                 16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
                 17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
                 18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
                 19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
                 20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
                 21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
                 22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
                 23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
                 24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
                 25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

     Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1383	100.0	1383	21	AAZ39386	Smooth muscle prol
2	1383	100.0	2429	21	AAZ39387	Smooth muscle prol
3	1383	100.0	2429	21	AAZ40031	Full length mouse
4	1327.4	96.0	1344	21	AAZ39383	Smooth muscle prol
5	1327.4	96.0	2233	21	AAZ39384	Smooth muscle prol
6	1327.4	96.0	2233	21	AAZ40029	Full length mouse
7	1269	91.8	1269	21	AAZ39385	Smooth muscle prol
8	1269	91.8	1269	21	AAZ39388	Smooth muscle prol
9	1098.6	79.4	1347	24	ABL52528	Human UP50 cDNA se
10	1098.6	79.4	1720	19	AAV62432	Human EEGF genomic
11	1098.6	79.4	1720	24	ABK13627	Human cDNA encodin
12	1098.6	79.4	2126	22	AAK94505	Human full-length
13	1098.6	79.4	2328	21	AAZ40027	Full length human
14	1098.6	79.4	2362	20	AAX07567	Homo sapiens fetal
15	1098.6	79.4	2362	21	AAZ39892	cDNA sequence of t
16	1098.6	79.4	2550	20	AAX05359	Human extracellula
17	1097	79.3	2509	20	AAX37670	Human EGF-like hom
18	1097	79.3	2609	22	AAS46128	Human DNA encoding
19	1097	79.3	2609	22	AAC86968	Nucleotide sequenc
20	1097	79.3	2609	25	ACA57886	Human PRO210 cDNA.
21	1097	79.3	2609	25	ACA60458	Novel human secret
22	1097	79.3	2609	25	ABX98356	Human cDNA encodin
23	1097	79.3	2609	25	ABX98858	Novel human secret
24	1097	79.3	2609	25	ACA04448	Novel human secret
25	1097	79.3	2609	25	ACA04928	Novel human secret
26	1097	79.3	2609	25	ACA05903	Human secreted/tra
27	1097	79.3	2609	25	ABX97947	Human PRO polynucl
28	1097	79.3	2609	25	ABX78731	Human PRO polynucl
29	1097	79.3	2609	25	ABX75744	Human cDNA encodin
30	1097	79.3	2609	25	ABX76949	Human PRO polynucl
31	1097	79.3	2609	25	ABX16789	Human cDNA encodin
32	1082.6	78.3	2019	24	ABT10172	Human breast cance
33	1000.8	72.4	1228	18	AAT89380	Human extracellula
34	922.2	66.7	1254	21	AAZ61672	cDNA encoding rat
35	922.2	66.7	1254	22	AAC99605	Skin cell cDNA, SE
36	920.2	66.5	1260	24	ABL34757	Rat cDNA isolated
37	650	47.0	778	20	AAX37673	Human PRO protein
38	604.6	43.7	853	22	AAK91596	Human cDNA 5'-end
39	604.6	43.7	853	22	AAK93169	Human cDNA clone r
40	604.6	43.7	1538	22	AAK94129	Human full-length
41	527.6	38.1	680	21	AAA44245	Human secreted exp
42	350.4	25.3	1707	22	AAH13771	Human cDNA sequenc
43	349.2	25.2	1480	21	AAA14608	cDNA encoding a hu
44	349.2	25.2	1525	18	AAT88974	Human extracellula
45	349.2	25.2	1531	20	AAX60351	Extracellular prot

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 12:56:44 ; Search time 92.7538 Seconds
                                               (without alignments)
                                               6581.220 Million cell updates/sec

Title: US-09-674-330A-6
Perfect score: 1383
Sequence: 1 atgggacctagaagtttcga..........atgtgtcgcagtatccgttc 1383

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

                         %
Result   Query
   No.   Score   Match Length DB ID   Description
----
     1   1098.6   79.4   2550   2 US-08-884-072-2   Sequence 2, Appli
     2   1098.6   79.4   2550   4 US-09-212-168-2   Sequence 2, Appli
     3   922.2   66.7   1254   4 US-09-312-283C-67   Sequence 67, Appl
     4   920.2   66.5   1260   3 US-09-188-930-67   Sequence 67, Appl
     5   349.2   25.2   1531   2 US-08-833-963C-1   Sequence 1, Appli
     6   347.6   25.1   2018   3 US-08-980-514-2   Sequence 2, Appli
     7   289.4   20.9   1018   3 US-09-188-930-259   Sequence 259, App
     8   289.4   20.9   1018   4 US-09-312-283C-259   Sequence 259, App
     9   244.6   17.7   2512   4 US-09-248-757-1   Sequence 1, Appli
    10   102.8   7.4   3373   2 US-08-897-443-2   Sequence 2, Appli
    11   92.4   6.7   401   4 US-09-643-597-278   Sequence 278, App

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 18:05:35 ; Search time 436.427 Seconds
                                               (without alignments)
                                               10532.199 Million cell updates/sec

Title: US-09-674-330A-6
Perfect score: 1383
Sequence: 1 atgggacctagaagtttcga..........atgtgtcgcagtatccgttc 1383

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                 1:   /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                 2:   /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                 3:   /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                 4:   /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                 5:   /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 6:   /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                 7:   /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                 8:   /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                 9:   /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
                 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
                 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
                 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

```
                              SUMMARIES
                   %
Result          Query
  No.   Score  Match Length DB  ID                      Description
      --------------------------------------------------------------------
       1   1217   88.0   2499  15  US-10-175-523-164     Sequence 164, App
       2  1098.6  79.4   1717   9  US-09-275-805-1       Sequence 1, Appli
       3  1098.6  79.4   2362   9  US-09-083-002-1       Sequence 1, Appli
       4  1098.6  79.4   2362  14  US-10-041-016-1       Sequence 1, Appli
       5  1098.6  79.4   2550   9  US-09-836-561-2       Sequence 2, Appli
       6   1097   79.3   2609  13  US-10-199-672-407     Sequence 407, App
       7   1097   79.3   2609  13  US-10-187-749-407     Sequence 407, App
       8   1097   79.3   2609  13  US-10-194-457-407     Sequence 407, App
       9   1097   79.3   2609  13  US-10-184-642-407     Sequence 407, App
      10   1097   79.3   2609  13  US-10-196-747-407     Sequence 407, App
      11   1097   79.3   2609  13  US-10-173-689-407     Sequence 407, App
      12   1097   79.3   2609  13  US-10-173-690-407     Sequence 407, App
      13   1097   79.3   2609  13  US-10-173-691-407     Sequence 407, App
      14   1097   79.3   2609  13  US-10-173-692-407     Sequence 407, App
      15   1097   79.3   2609  13  US-10-173-694-407     Sequence 407, App
      16   1097   79.3   2609  13  US-10-173-698-407     Sequence 407, App
      17   1097   79.3   2609  13  US-10-173-699-407     Sequence 407, App
      18   1097   79.3   2609  13  US-10-173-707-407     Sequence 407, App
      19   1097   79.3   2609  13  US-10-174-569-407     Sequence 407, App
      20   1097   79.3   2609  13  US-10-174-583-407     Sequence 407, App
      21   1097   79.3   2609  13  US-10-174-587-407     Sequence 407, App
      22   1097   79.3   2609  13  US-10-174-589-407     Sequence 407, App
      23   1097   79.3   2609  13  US-10-174-591-407     Sequence 407, App
      24   1097   79.3   2609  13  US-10-175-736-407     Sequence 407, App
      25   1097   79.3   2609  13  US-10-175-742-407     Sequence 407, App
      26   1097   79.3   2609  13  US-10-175-744-407     Sequence 407, App
      27   1097   79.3   2609  13  US-10-175-745-407     Sequence 407, App
      28   1097   79.3   2609  13  US-10-175-748-407     Sequence 407, App
      29   1097   79.3   2609  13  US-10-175-751-407     Sequence 407, App
      30   1097   79.3   2609  13  US-10-175-754-407     Sequence 407, App
      31   1097   79.3   2609  13  US-10-176-480-407     Sequence 407, App
      32   1097   79.3   2609  13  US-10-176-489-407     Sequence 407, App
      33   1097   79.3   2609  13  US-10-176-754-407     Sequence 407, App
      34   1097   79.3   2609  13  US-10-176-755-407     Sequence 407, App
      35   1097   79.3   2609  13  US-10-176-759-407     Sequence 407, App
      36   1097   79.3   2609  13  US-10-176-920-407     Sequence 407, App
      37   1097   79.3   2609  13  US-10-176-922-407     Sequence 407, App
      38   1097   79.3   2609  13  US-10-176-924-407     Sequence 407, App
      39   1097   79.3   2609  13  US-10-176-984-407     Sequence 407, App
      40   1097   79.3   2609  13  US-10-179-508-407     Sequence 407, App
      41   1097   79.3   2609  13  US-10-179-512-407     Sequence 407, App
      42   1097   79.3   2609  13  US-10-179-515-407     Sequence 407, App
      43   1097   79.3   2609  13  US-10-066-198-14      Sequence 14, Appl
      44   1097   79.3   2609  13  US-10-173-702-407     Sequence 407, App
      45   1097   79.3   2609  13  US-10-173-703-407     Sequence 407, App


                              ALIGNMENTS



RESULT 1
US-10-175-523-164
```

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 12:45:39 ; Search time 2707.86 Seconds
                                             (without alignments)
                                             12413.176 Million cell updates/sec

Title: US-09-674-330A-6
Perfect score: 1383
Sequence: 1 atgggacctagaagtttcga..........atgtgtcgcagtatccgttc 1383

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1:   em_estba:*
                 2:   em_esthum:*
                 3:   em_estin:*
                 4:   em_estmu:*
                 5:   em_estov:*
                 6:   em_estpl:*
                 7:   em_estro:*
                 8:   em_htc:*
                 9:   gb_est1:*
                 10: gb_est2:*
                 11: gb_htc:*
                 12: gb_est3:*
                 13: gb_est4:*
                 14: gb_est5:*
                 15: em_estfun:*
                 16: em_estom:*
                 17: em_gss_hum:*
                 18: em_gss_inv:*
                 19: em_gss_pln:*
                 20: em_gss_vrt:*
                 21: em_gss_fun:*
                 22: em_gss_mam:*
                 23: em_gss_mus:*
                 24: em_gss_pro:*
                 25: em_gss_rod:*
                 26: em_gss_phg:*
                 27: em_gss_vrl:*

```
        28:  gb_gss1:*
        29:  gb_gss2:*


Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                    SUMMARIES
                     %
Result          Query
    No.   Score  Match Length DB   ID                   Description
    ------------------------------------------------------------------------------
      1  1327.4   96.0   1835  11   AK085170             AK085170 Mus muscu
      2  1327.4   96.0   5831  11   AK090129             AK090129 Mus muscu
      3  1017.2   73.6   2423  11   CNSLT1I9S            BX248290 human ful
      4   760.8   55.0    796  12   BI453348             BI453348 603173067
      5   754.4   54.5    980  13   BU520272             BU520272 AGENCOURT
      6   745.2   53.9    870  13   BQ930927             BQ930927 AGENCOURT
      7   724.6   52.4   1796  11   AK084895             AK084895 Mus muscu
      8   716     51.8   1201  13   BX439363             BX439363 BX439363
      9   708     51.2    717  12   BI251219             BI251219 602994427
     10   691.4   50.0   1014  12   BM921371             BM921371 AGENCOURT
     11   689.4   49.8    912  13   BU149085             BU149085 AGENCOURT
     12   679     49.1    877  13   BX326257             BX326257 BX326257
     13   678.2   49.0    842  13   BX367825             BX367825 BX367825
     14   672.8   48.6    996  13   BQ720516             BQ720516 AGENCOURT
     15   666.2   48.2    815  10   BG174360             BG174360 602336371
     16   660.8   47.8    888  13   BX346924             BX346924 BX346924
     17   655.8   47.4    841  14   CD172152             CD172152 AGENCOURT
     18   649.4   47.0    954  12   BM545444             BM545444 AGENCOURT
     19   643.4   46.5    904  13   BQ716569             BQ716569 AGENCOURT
     20   642.6   46.5    952  13   BU148724             BU148724 AGENCOURT
     21   641.6   46.4    930  13   BX349066             BX349066 BX349066
     22   636.6   46.0    854  13   BX347366             BX347366 BX347366
  c  23   634.8   45.9    870  13   BX429526             BX429526 BX429526
     24   600     43.4    762  14   CB595725             CB595725 AGENCOURT
  c  25   580.4   42.0    923  13   BX326104             BX326104 BX326104
  c  26   580.2   42.0    954  13   BX371974             BX371974 BX371974
     27   562.4   40.7    654  14   CB595181             CB595181 AGENCOURT
  c  28   557.4   40.3    906  13   BX388741             BX388741 BX388741
     29   557.2   40.3    914  13   BX450129             BX450129 BX450129
     30   556     40.2    822  10   BG109391             BG109391 602280448
     31   554.4   40.1   1101  10   BG245848             BG245848 602358649
     32   550.6   39.8    891  10   BF339448             BF339448 602039102
     33   538.8   39.0    867  13   BX326018             BX326018 BX326018
     34   535     38.7    778  13   BU750981             BU750981 CH3#037_B
     35   531.2   38.4    894  13   BX408562             BX408562 BX408562
     36   530.4   38.4    644  12   BG938621             BG938621 cn27c11.x
     37   503     36.4    882  12   BI825121             BI825121 603038662
     38   487.6   35.3    835  13   BQ718885             BQ718885 AGENCOURT
     39   482.2   34.9    627  12   BI183862             BI183862 UNL-P-FN-
     40   482     34.9    880  12   BI764020             BI764020 603043221
  c  41   481.4   34.8    627  10   BF090699             BF090699 QV2-NT004
     42   472.8   34.2    680   9   AW106432             AW106432 um27g01.y
     43   472.4   34.2    933  13   BQ716088             BQ716088 AGENCOURT
     44   470     34.0    912  12   BI768516             BI768516 603057118
     45   469.6   34.0    636  14   BY753400             BY753400 BY753400
```

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 07:36:19 ; Search time 4585.99 Seconds
                                              (without alignments)
                                              11320.190 Million cell updates/sec

Title: US-09-674-330A-10
Perfect score: 1269
Sequence: 1 cagtgcacaaacggcttttga..........atgtgtcgcagtatccgttc 1269

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*
                 15: em_ba:*
                 16: em_fun:*
                 17: em_hum:*
                 18: em_in:*
                 19: em_mu:*
                 20: em_om:*
                 21: em_or:*
                 22: em_ov:*
                 23: em_pat:*
                 24: em_ph:*
                 25: em_pl:*
                 26: em_ro:*
                 27: em_sts:*

```
28:   em_un:*
29:   em_vi:*
30:   em_htg_hum:*
31:   em_htg_inv:*
32:   em_htg_other:*
33:   em_htg_mus:*
34:   em_htg_pln:*
35:   em_htg_rod:*
36:   em_htg_mam:*
37:   em_htg_vrt:*
38:   em_sy:*
39:   em_htgo_hum:*
40:   em_htgo_mus:*
41:   em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1269	100.0	2230	10	BC006636	BC006636 Mus muscu
2	1269	100.0	2478	10	AF112151	AF112151 Mus muscu
3	1165	91.8	2499	10	AF112153	AF112153 Rattus no
4	1163.4	91.7	2304	10	AF137350	AF137350 Rattus no
5	1056.2	83.2	1720	6	A84086	A84086 Sequence 1
6	1056.2	83.2	2019	9	HSA133490	AJ133490 Homo sapi
7	1056.2	83.2	2126	6	BD127534	BD127534 Primer fo
8	1056.2	83.2	2126	9	AK075147	AK075147 Homo sapi
9	1056.2	83.2	2328	9	AF112152	AF112152 Homo sapi
10	1056.2	83.2	2367	9	BC022280	BC022280 Homo sapi
11	1056.2	83.2	2550	6	AR036548	AR036548 Sequence
12	1056.2	83.2	2550	6	AR173204	AR173204 Sequence
13	1056.2	83.2	2550	6	BD132822	BD132822 human ext
14	1054.6	83.1	2609	6	AX376340	AX376340 Sequence
15	1054.6	83.1	2609	6	AX403659	AX403659 Sequence
16	1040.2	82.0	2019	9	AF093118	AF093118 Homo sapi
17	604.6	47.6	853	6	BD124625	BD124625 Primer fo
18	604.6	47.6	853	6	BD126198	BD126198 Primer fo
19	604.6	47.6	1538	6	BD127158	BD127158 Primer fo
20	604.6	47.6	1538	9	AK074540	AK074540 Homo sapi
21	350.4	27.6	1440	9	HSA132819	AJ132819 Homo sapi
22	350.4	27.6	1536	9	AB030655	AB030655 Homo sapi
23	350	27.6	1707	6	BD155763	BD155763 Primer fo
24	350	27.6	1707	9	AK000980	AK000980 Homo sapi
25	348.8	27.5	1480	6	AX023967	AX023967 Sequence
26	348.8	27.5	1561	9	BC010456	BC010456 Homo sapi
27	348.8	27.5	1866	9	AK075453	AK075453 Homo sapi
28	347.2	27.4	1757	6	AX577988	AX577988 Sequence
29	347.2	27.4	1757	9	AF109121	AF109121 Homo sapi
30	347.2	27.4	1875	6	AX201326	AX201326 Sequence
31	347.2	27.4	1875	6	AX464184	AX464184 Sequence
32	347.2	27.4	2018	6	AR095382	AR095382 Sequence
33	344	27.1	1350	6	AX577913	AX577913 Sequence

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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 21:43:31 ; Search time 324.236 Seconds
                                                 (without alignments)
                                                 10565.088 Million cell updates/sec

Title: US-09-674-330A-10
Perfect score: 1269
Sequence: 1 cagtgcacaaacggctttga..........atgtgtcgcagtatccgttc 1269

Scoring table: IDENTITY_NUC
                    Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_19Jun03:*
                    1:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
                    2:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
                    3:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
                    4:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
                    5:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
                    6:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
                    7:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
                    8:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
                    9:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
                   10:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
                   11:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
                   12:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
                   13:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
                   14:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
                   15:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
                   16:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
                   17:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
                   18:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
                   19:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
                   20:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
                   21:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
                   22:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
                   23:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
                   24:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
                   25:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

     Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

<div align="center">SUMMARIES</div>

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1269	100.0	1269	21	AAZ39385	Smooth muscle prol
2	1269	100.0	1269	21	AAZ39388	Smooth muscle prol
3	1269	100.0	1344	21	AAZ39383	Smooth muscle prol
4	1269	100.0	1383	21	AAZ39386	Smooth muscle prol
5	1269	100.0	2233	21	AAZ39384	Smooth muscle prol
6	1269	100.0	2233	21	AAZ40029	Full length mouse
7	1269	100.0	2429	21	AAZ39387	Smooth muscle prol
8	1269	100.0	2429	21	AAZ40031	Full length mouse
9	1056.2	83.2	1347	24	ABL52528	Human UP50 cDNA se
10	1056.2	83.2	1720	19	AAV62432	Human EEGF genomic
11	1056.2	83.2	1720	24	ABK13627	Human cDNA encodin
12	1056.2	83.2	2126	22	AAK94505	Human full-length
13	1056.2	83.2	2328	21	AAZ40027	Full length human
14	1056.2	83.2	2362	20	AAX07567	Homo sapiens fetal
15	1056.2	83.2	2362	21	AAZ39892	cDNA sequence of t
16	1056.2	83.2	2550	20	AAX05359	Human extracellula
17	1054.6	83.1	2509	20	AAX37670	Human EGF-like hom
18	1054.6	83.1	2609	22	AAS46128	Human DNA encoding
19	1054.6	83.1	2609	22	AAC86968	Nucleotide sequenc
20	1054.6	83.1	2609	25	ACA57886	Human PRO210 cDNA.
21	1054.6	83.1	2609	25	ACA60458	Novel human secret
22	1054.6	83.1	2609	25	ABX98356	Human cDNA encodin
23	1054.6	83.1	2609	25	ABX98858	Novel human secret
24	1054.6	83.1	2609	25	ACA04448	Novel human secret
25	1054.6	83.1	2609	25	ACA04928	Novel human secret
26	1054.6	83.1	2609	25	ACA05903	Human secreted/tra
27	1054.6	83.1	2609	25	ABX97947	Human PRO polynucl
28	1054.6	83.1	2609	25	ABX78731	Human PRO polynucl
29	1054.6	83.1	2609	25	ABX75744	Human cDNA encodin
30	1054.6	83.1	2609	25	ABX76949	Human PRO polynucl
31	1054.6	83.1	2609	25	ABX16789	Human cDNA encodin
32	1040.2	82.0	2019	24	ABT10172	Human breast cance
33	1000.8	78.9	1228	18	AAT89380	Human extracellula
34	922.2	72.7	1254	21	AAZ61672	cDNA encoding rat
35	922.2	72.7	1254	22	AAC99605	Skin cell cDNA, SE
36	920.2	72.5	1260	24	ABL34757	Rat cDNA isolated
37	650	51.2	778	20	AAX37673	Human PRO protein
38	604.6	47.6	853	22	AAK91596	Human cDNA 5'-end
39	604.6	47.6	853	22	AAK93169	Human cDNA clone r
40	604.6	47.6	1538	22	AAK94129	Human full-length
41	472.8	37.3	680	21	AAA44245	Human secreted exp
42	350	27.6	1707	22	AAH13771	Human cDNA sequenc
43	348.8	27.5	1480	21	AAA14608	cDNA encoding a hu
44	348.8	27.5	1525	18	AAT88974	Human extracellula
45	348.8	27.5	1531	20	AAX60351	Extracellular prot

<div align="center">ALIGNMENTS</div>

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 12:56:44 ; Search time 85.1081 Seconds
                                              (without alignments)
                                              6581.220 Million cell updates/sec

Title: US-09-674-330A-10
Perfect score: 1269
Sequence: 1 cagtgcacaaacggctttga..........atgtgtcgcagtatccgttc 1269

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
   No.   Score Match Length DB ID   Description
----
     1   1056.2   83.2   2550 2 US-08-884-072-2   Sequence 2, Appli
     2   1056.2   83.2   2550 4 US-09-212-168-2   Sequence 2, Appli
     3   922.2   72.7   1254 4 US-09-312-283C-67   Sequence 67, Appl
     4   920.2   72.5   1260 3 US-09-188-930-67   Sequence 67, Appl
     5   348.8   27.5   1531 2 US-08-833-963C-1   Sequence 1, Appli
     6   347.2   27.4   2018 3 US-08-980-514-2   Sequence 2, Appli
     7   289.4   22.8   1018 3 US-09-188-930-259   Sequence 259, App
     8   289.4   22.8   1018 4 US-09-312-283C-259   Sequence 259, App
     9   244.6   19.3   2512 4 US-09-248-757-1   Sequence 1, Appli
    10   102.8   8.1   3373 2 US-08-897-443-2   Sequence 2, Appli
    11   92.4   7.3   401 4 US-09-643-597-278   Sequence 278, App

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 18:05:35 ; Search time 400.453 Seconds
                                               (without alignments)
                                               10532.199 Million cell updates/sec

Title: US-09-674-330A-10
Perfect score: 1269
Sequence: 1 cagtgcacaaacggctttga..........atgtgtcgcagtatccgttc 1269

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
           1:    /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
           2:    /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
           3:    /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
           4:    /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
           5:    /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
           6:    /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
           7:    /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
           8:    /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
           9:    /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
          10:    /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
          11:    /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
          12:    /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
          13:    /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
          14:    /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
          15:    /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
          16:    /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
          17:    /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
          18:    /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1165	91.8	2499	15	US-10-175-523-164	Sequence 164, App
2	1056.2	83.2	1717	9	US-09-275-805-1	Sequence 1, Appli
3	1056.2	83.2	2362	9	US-09-083-002-1	Sequence 1, Appli
4	1056.2	83.2	2362	14	US-10-041-016-1	Sequence 1, Appli
5	1056.2	83.2	2550	9	US-09-836-561-2	Sequence 2, Appli
6	1054.6	83.1	2609	13	US-10-199-672-407	Sequence 407, App
7	1054.6	83.1	2609	13	US-10-187-749-407	Sequence 407, App
8	1054.6	83.1	2609	13	US-10-194-457-407	Sequence 407, App
9	1054.6	83.1	2609	13	US-10-184-642-407	Sequence 407, App
10	1054.6	83.1	2609	13	US-10-196-747-407	Sequence 407, App
11	1054.6	83.1	2609	13	US-10-173-689-407	Sequence 407, App
12	1054.6	83.1	2609	13	US-10-173-690-407	Sequence 407, App
13	1054.6	83.1	2609	13	US-10-173-691-407	Sequence 407, App
14	1054.6	83.1	2609	13	US-10-173-692-407	Sequence 407, App
15	1054.6	83.1	2609	13	US-10-173-694-407	Sequence 407, App
16	1054.6	83.1	2609	13	US-10-173-698-407	Sequence 407, App
17	1054.6	83.1	2609	13	US-10-173-699-407	Sequence 407, App
18	1054.6	83.1	2609	13	US-10-173-707-407	Sequence 407, App
19	1054.6	83.1	2609	13	US-10-174-569-407	Sequence 407, App
20	1054.6	83.1	2609	13	US-10-174-583-407	Sequence 407, App
21	1054.6	83.1	2609	13	US-10-174-587-407	Sequence 407, App
22	1054.6	83.1	2609	13	US-10-174-589-407	Sequence 407, App
23	1054.6	83.1	2609	13	US-10-174-591-407	Sequence 407, App
24	1054.6	83.1	2609	13	US-10-175-736-407	Sequence 407, App
25	1054.6	83.1	2609	13	US-10-175-742-407	Sequence 407, App
26	1054.6	83.1	2609	13	US-10-175-744-407	Sequence 407, App
27	1054.6	83.1	2609	13	US-10-175-745-407	Sequence 407, App
28	1054.6	83.1	2609	13	US-10-175-748-407	Sequence 407, App
29	1054.6	83.1	2609	13	US-10-175-751-407	Sequence 407, App
30	1054.6	83.1	2609	13	US-10-175-754-407	Sequence 407, App
31	1054.6	83.1	2609	13	US-10-176-480-407	Sequence 407, App
32	1054.6	83.1	2609	13	US-10-176-489-407	Sequence 407, App
33	1054.6	83.1	2609	13	US-10-176-754-407	Sequence 407, App
34	1054.6	83.1	2609	13	US-10-176-755-407	Sequence 407, App
35	1054.6	83.1	2609	13	US-10-176-759-407	Sequence 407, App
36	1054.6	83.1	2609	13	US-10-176-920-407	Sequence 407, App
37	1054.6	83.1	2609	13	US-10-176-922-407	Sequence 407, App
38	1054.6	83.1	2609	13	US-10-176-924-407	Sequence 407, App
39	1054.6	83.1	2609	13	US-10-176-984-407	Sequence 407, App
40	1054.6	83.1	2609	13	US-10-179-508-407	Sequence 407, App
41	1054.6	83.1	2609	13	US-10-179-512-407	Sequence 407, App
42	1054.6	83.1	2609	13	US-10-179-515-407	Sequence 407, App
43	1054.6	83.1	2609	13	US-10-066-198-14	Sequence 14, Appl
44	1054.6	83.1	2609	13	US-10-173-702-407	Sequence 407, App
45	1054.6	83.1	2609	13	US-10-173-703-407	Sequence 407, App

ALIGNMENTS

RESULT 1
US-10-175-523-164

OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 12:45:39 ; Search time 2484.65 Seconds
                                              (without alignments)
                                              12413.176 Million cell updates/sec

Title: US-09-674-330A-10
Perfect score: 1269
Sequence: 1 cagtgcacaaacggctttga..........atgtgtcgcagtatccgttc 1269

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                   1: em_estba:*
                   2: em_esthum:*
                   3: em_estin:*
                   4: em_estmu:*
                   5: em_estov:*
                   6: em_estpl:*
                   7: em_estro:*
                   8: em_htc:*
                   9: gb_est1:*
                   10: gb_est2:*
                   11: gb_htc:*
                   12: gb_est3:*
                   13: gb_est4:*
                   14: gb_est5:*
                   15: em_estfun:*
                   16: em_estom:*
                   17: em_gss_hum:*
                   18: em_gss_inv:*
                   19: em_gss_pln:*
                   20: em_gss_vrt:*
                   21: em_gss_fun:*
                   22: em_gss_mam:*
                   23: em_gss_mus:*
                   24: em_gss_pro:*
                   25: em_gss_rod:*
                   26: em_gss_phg:*
                   27: em_gss_vrl:*

```
        28:  gb_gss1:*
        29:  gb_gss2:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

<div align="center">SUMMARIES</div>

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1269	100.0	1835	11	AK085170	AK085170 Mus muscu
	2	1269	100.0	5831	11	AK090129	AK090129 Mus muscu
	3	1017.2	80.2	2423	11	CNSLT1I9S	BX248290 human ful
	4	760.8	60.0	796	12	BI453348	BI453348 603173067
	5	708	55.8	717	12	BI251219	BI251219 602994427
	6	696	54.8	980	13	BU520272	BU520272 AGENCOURT
	7	686.8	54.1	870	13	BQ930927	BQ930927 AGENCOURT
	8	679	53.5	877	13	BX326257	BX326257 BX326257
	9	678.2	53.4	842	13	BX367825	BX367825 BX367825
	10	673.6	53.1	1201	13	BX439363	BX439363 BX439363
	11	666.2	52.5	1796	11	AK084895	AK084895 Mus muscu
	12	660.8	52.1	888	13	BX346924	BX346924 BX346924
	13	659.6	52.0	996	13	BQ720516	BQ720516 AGENCOURT
	14	655.8	51.7	841	14	CD172152	CD172152 AGENCOURT
	15	649.4	51.2	954	12	BM545444	BM545444 AGENCOURT
	16	649	51.1	1014	12	BM921371	BM921371 AGENCOURT
	17	643.4	50.7	904	13	BQ716569	BQ716569 AGENCOURT
	18	642.6	50.6	952	13	BU148724	BU148724 AGENCOURT
	19	641.6	50.6	930	13	BX349066	BX349066 BX349066
	20	636.6	50.2	854	13	BX347366	BX347366 BX347366
c	21	634.8	50.0	870	13	BX429526	BX429526 BX429526
	22	631	49.7	912	13	BU149085	BU149085 AGENCOURT
	23	607.8	47.9	815	10	BG174360	BG174360 602336371
	24	600	47.3	762	14	CB595725	CB595725 AGENCOURT
c	25	580.4	45.7	923	13	BX326104	BX326104 BX326104
c	26	580.2	45.7	954	13	BX371974	BX371974 BX371974
	27	562.4	44.3	654	14	CB595181	CB595181 AGENCOURT
c	28	557.4	43.9	906	13	BX388741	BX388741 BX388741
	29	557.2	43.9	914	13	BX450129	BX450129 BX450129
	30	556	43.8	822	10	BG109391	BG109391 602280448
	31	550.6	43.4	891	10	BF339448	BF339448 602039102
	32	538.8	42.5	867	13	BX326018	BX326018 BX326018
	33	535	42.2	778	13	BU750981	BU750981 CH3#037_B
	34	531.2	41.9	894	13	BX408562	BX408562 BX408562
	35	530.4	41.8	644	12	BG938621	BG938621 cn27c11.x
	36	482.2	38.0	627	12	BI183862	BI183862 UNL-P-FN-
c	37	481.4	37.9	627	10	BF090699	BF090699 QV2-NT004
	38	472.4	37.2	933	13	BQ716088	BQ716088 AGENCOURT
	39	470	37.0	912	12	BI768516	BI768516 603057118
	40	462.4	36.4	803	13	BU356104	BU356104 603476062
	41	462	36.4	462	10	BE656312	BE656312 UI-M-BH0-
	42	460.6	36.3	882	12	BI825121	BI825121 603038662
	43	454.8	35.8	576	9	AW142226	AW142226 EST292462
	44	452	35.6	1022	13	BU150258	BU150258 AGENCOURT
	45	449.8	35.4	745	10	BG431026	BG431026 602498636